

OM protein - protein search, using sw model

Run on: May 17, 2004, 11:10:57 ; Search time 52.6444 Seconds
(without alignments)
740.659 Million cell updates/sec

Title: US-10-010-942B-4
Perfect score: 719
Sequence: 1 MNFGLSLIFLVLVLKGVQCE.....DHYSGSSDYWGQGT'TVTVSS 138

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	718	99.9	138	5	ABG76924	Abg76924 Mouse 3D6
2	652	90.7	138	5	ABG76928	Abg76928 Humanised
3	651	90.5	468	6	ABP58275	Abp58275 Humanised
4	650	90.4	138	5	ABG76932	Abg76932 Humanised
5	609.5	84.8	133	6	ABG74243	Abg74243 Mouse ant
6	578.5	80.5	139	6	ABG74247	Abg74247 Mouse ant
7	578	80.4	462	6	AAO29869	Aao29869 Mouse ant
8	578	80.4	464	5	AAU72801	Aau72801 TRA-8 hea
9	573	79.7	138	2	AAR20064	Aar20064 MRK16-H c

10	569	79.1	144	5	ABB79730	Abb79730	Anti-Stre
11	568	79.0	139	2	AAR30480	Aar30480	hCEA spec
12	566	78.7	140	5	AAU76122	Aau76122	Mouse mon
13	564	78.4	139	2	AAR27053	Aar27053	Anti-CEA
14	564	78.4	140	5	AAU76133	Aau76133	Mouse mAb
15	563	78.3	138	2	AAW03722	Aaw03722	Anti-huma
16	561	78.0	140	5	AAU76132	Aau76132	Mouse mAb
17	560	77.9	138	3	AAV32404	Aay32404	Mouse ant
18	559	77.7	140	6	ABG74241	Abg74241	Mouse ant
19	557.5	77.5	137	2	AAW57592	Aaw57592	Chimeric
20	557.5	77.5	137	2	AAW89625	Aaw89625	Mouse hum
21	557.5	77.5	137	3	AAV77513	Aay77513	Mouse ant
22	557.5	77.5	137	4	AAG67102	Aag67102	Amino aci
23	557.5	77.5	137	4	AAG64775	Aag64775	Mouse ant
24	557.5	77.5	137	4	AAG63393	Aag63393	Amino aci
25	557.5	77.5	137	5	ABB95208	Abb95208	Mouse joi
26	557.5	77.5	137	6	ABJ36667	Abj36667	Angiogene
27	557	77.5	119	6	ABP58271	Abp58271	Humanised
28	557	77.5	449	6	ABP58273	Abp58273	Humanised
29	554.5	77.1	139	1	AAP90480	Aap90480	Chimeric
30	551	76.6	119	6	ABP58269	Abp58269	Humanised
31	551	76.6	158	2	AAW19579	Aaw19579	Mouse ant
32	551	76.6	477	2	AAR47450	Aar47450	T84.12 He
33	551	76.6	477	2	AAR47453	Aar47453	chiT84.12
34	549	76.4	140	2	AAW21841	Aaw21841	Heavy cha
35	549	76.4	247	2	AAW11917	Aaw11917	Murine MA
36	545	75.8	142	2	AAR30882	Aar30882	Antibody
37	542	75.4	140	7	ADC24966	Adc24966	Murine G2
38	539	75.0	136	2	AAR06251	Aar06251	Variable
39	539	75.0	138	3	AAV32406	Aay32406	Mouse ant
40	537	74.7	159	4	AAU14226	Aau14226	Human nov
41	535	74.4	138	2	AAR32246	Aar32246	BR55-2 mu
42	535	74.4	138	2	AAR32242	Aar32242	Chimeric
43	535	74.4	139	2	AAR31588	Aar31588	BR55-2 he
44	535	74.4	158	2	AAW19577	Aaw19577	Mouse ant
45	534.5	74.3	139	2	AAR52773	Aar52773	Murine KC

ALIGNMENTS

RESULT 1

ABG76924

ID ABG76924 standard; protein; 138 AA.

XX

AC ABG76924;

XX

DT 05-NOV-2002 (first entry)

XX

DE Mouse 3D6 VH protein.

XX

KW Mouse; humanized; immunoglobulin; Ig; light chain; LC; heavy chain; HC;

KW variable region complementarity determining region; 3D6; 10D5;

KW variable framework region; amyloidogenic disease; Alzheimer's disease;

KW amyloid deposit; variable light chain; VL; variable heavy chain; VH;

KW nootropic; neuroprotective; inhibitor of beta amyloid accumulation;

KW Abeta.

XX
 OS Mus musculus.
 XX
 PN WO200246237-A2.
 XX
 PD 13-JUN-2002.
 XX
 PF 06-DEC-2001; 2001WO-US046587.
 XX
 PR 06-DEC-2000; 2000US-0251892P.
 XX
 PA (NEUR-) NEURALAB LTD.
 PA (AMHP) WYETH.
 XX
 PI Basi G, Saldanha J, Yednock T;
 XX
 DR WPI; 2002-519658/55.
 DR N-PSDB; ABS59427.
 XX
 PT Novel light/heavy chain of humanized immunoglobulin for treating
 PT amyloidogenic disease, has 3D6/10D5 variable region complementarity
 PT determining regions and variable framework region from human acceptor
 PT immunoglobulin.
 XX
 PS Claim 68; Fig 2; 171pp; English.
 XX
 CC The present invention relates to new humanized immunoglobulin (Ig) light
 CC chain (LC) or heavy chain (HC) comprising variable region complementarity
 CC determining regions from 3D6/10D5 Ig LC or HC variable region sequence,
 CC and variable framework region from human acceptor Ig LC or HC sequence.
 CC The invention is useful for preventing or treating an amyloidogenic
 CC disease or Alzheimer's disease in a patient. The invention is also useful
 CC for in vivo imaging amyloid deposits in a patient. The present amino acid
 CC sequence represents a mouse 3D6/10D5 variable light (VL) chain or
 CC variable heavy (VH) chain protein of the invention
 XX
 SQ Sequence 138 AA;

Query Match 99.9%; Score 718; DB 5; Length 138;
 Best Local Similarity 99.3%; Pred. No. 5.4e-57;
 Matches 137; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60

 Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120

 Qy 121 YSGSSDYWGQGTITVTVSS 138
 |||||||||:||||
 Db 121 YSGSSDYWGQGTITVTVSS 138

RESULT 2
 ABG76928

ID ABG76928 standard; protein; 138 AA.
 XX
 AC ABG76928;
 XX
 DT 05-NOV-2002 (first entry)
 XX
 DE Humanised 3D6 heavy chain variable region #1.
 XX
 KW Mouse; humanized; immunoglobulin; Ig; light chain; LC; heavy chain; HC;
 KW variable region complementarity determining region; 3D6; 10D5;
 KW variable framework region; amyloidogenic disease; Alzheimer's disease;
 KW amyloid deposit; variable light chain; VL; variable heavy chain; VH;
 KW nootropic; neuroprotective; inhibitor of beta amyloid accumulation;
 KW Abeta.
 XX
 OS Homo sapiens.
 OS Mus musculus.
 OS Synthetic.
 XX
 PN WO200246237-A2.
 XX
 PD 13-JUN-2002.
 XX
 PF 06-DEC-2001; 2001WO-US046587.
 XX
 PR 06-DEC-2000; 2000US-0251892P.
 XX
 PA (NEUR-) NEURALAB LTD.
 PA (AMHP) WYETH.
 XX
 PI Basi G, Saldanha J, Yednock T;
 XX
 DR WPI; 2002-519658/55.
 XX
 PT Novel light/heavy chain of humanized immunoglobulin for treating
 PT amyloidogenic disease, has 3D6/10D5 variable region complementarity
 PT determining regions and variable framework region from human acceptor
 PT immunoglobulin.
 XX
 PS Claim 54; Page 155; 171pp; English.
 XX
 CC The present invention relates to new humanized immunoglobulin (Ig) light
 CC chain (LC) or heavy chain (HC) comprising variable region complementarity
 CC determining regions from 3D6/10D5 Ig LC or HC variable region sequence,
 CC and variable framework region from human acceptor Ig LC or HC sequence.
 CC The invention is useful for preventing or treating an amyloidogenic
 CC disease or Alzheimer's disease in a patient. The invention is also useful
 CC for in vivo imaging amyloid deposits in a patient. The present amino acid
 CC sequence represents a humanized 3D6 variable light (VL) chain or variable
 CC heavy (VH) chain protein of the invention
 XX
 SQ Sequence 138 AA;

Query Match 90.7%; Score 652; DB 5; Length 138;
 Best Local Similarity 89.1%; Pred. No. 4.8e-51;
 Matches 123; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
 |||:|||||:| ||:|||||
 Db 1 MNFGLSLIFLVVLKGVQCEVQLLESGGGLVQPGGSLRLSCAASGFTFSNYGMSWVRQAP 60
 Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
 | |||:|||||:||||:|:|
 Db 61 GKGLEWVASIRSGGGRTYYSDNVKGRFTISRDNAKNSLYLQMNSLRAEDTALYYCVRYDH 120
 Qy 121 YSGSSDYWGQGTTVTVSS 138
 ||| |||
 Db 121 YSGSSDYWGQGTTLVTVSS 138

RESULT 3

ABP58275

ID ABP58275 standard; protein; 468 AA.

XX

AC ABP58275;

XX

DT 23-OCT-2003 (revised)

DT 31-MAR-2003 (first entry)

XX

DE Humanised 3D6 antibody heavy chain.

XX

KW Monoclonal antibody; 3D6; complementarity determining region; CDR; mouse;

KW human; humanised antibody; antibody; Alzheimer's disease;

KW Down's syndrome; cerebral amyloid angiopathy; neuroprotective; nootropic.

XX

OS Mus sp.

OS Homo sapiens.

OS Chimeric.

XX

FH	Key	Location/Qualifiers
----	-----	---------------------

FT	Peptide	1. .19
----	---------	--------

FT		/label= Signal_peptide
----	--	------------------------

FT	Protein	20. .468
----	---------	----------

FT		/label= Mature_peptide
----	--	------------------------

FT		/note= "the mature heavy chain is claimed in Claim 5"
----	--	---

FT	Region	20. .138
----	--------	----------

FT		/note= "heavy chain variable region, claimed in Claim 4"
----	--	--

FT	Region	50. .54
----	--------	---------

FT		/note= "CDR1"
----	--	---------------

FT	Region	69. .85
----	--------	---------

FT		/note= "CDR2"
----	--	---------------

FT	Region	118. .127
----	--------	-----------

FT		/note= "CDR3"
----	--	---------------

XX

PN WO200288306-A2.

XX

PD 07-NOV-2002.

XX

PF 26-APR-2002; 2002WO-US011853.

XX

PR 30-APR-2001; 2001US-0287539P.

XX

PA (ELIL) LILLY & CO ELI.

XX

PI Tsurushita N, Vasquez M;
XX
DR WPI; 2003-183835/18.
DR N-PSDB; ABZ24633, ABZ24635.

The present sequence is that of a preferred heavy chain of a humanised antibody of the present invention. In the variable region of this sequence, the complementarity determining regions (CDRs) originate from murine monoclonal antibody 3D6 and the framework region from human germline VH segment DP-45 and J segment JH4. Novel humanised antibodies of the invention have CDRs from 3D6 and human framework sequences. These humanised antibodies have binding affinities (affinity and epitope location) approximately the same as those of the mouse 3D6 antibody. The invention includes antibodies, single chain antibodies, and their fragments, as well as nucleotide sequences, vectors, transformed host cells, and methods of using the humanised antibody to treat, prevent, alleviate, reverse or otherwise ameliorate symptoms and/or pathology associated with Down's syndrome, (pre-)clinical Alzheimer's disease or (pre-)clinical cerebral amyloid angiopathy, and to inhibit formation or reduce Abeta plaque in the brain. (Updated on 23-OCT-2003 to standardise OS field)

SO Sequence 468 AA;

Query Match 90.5%; Score 651; DB 6; Length 468;
Best Local Similarity 89.1%; Pred. No. 2.4e-50;
Matches 123; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

Qy	1	MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS	60
Db	1	MNFGLSLIFLVLVLKGVQCEVQLVESGGGLVQPGGSLRLSCAGSGFTFSNYGMSWVRQAP	60
Qy	61	DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH	120
Db	61	GKGLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNSLYLQMNSLRAEDTAVYYCVRYDH	120
Qy	121	YSGSSDYWGQGTTLTVSS	138
Db	121	YSGSSDYWGQGTTLTVSS	138

RESULT 4

ABG76932

ID ABG76932 standard; protein; 138 AA.

XX

AC ABG76932;

XX

DT 05-NOV-2002 (first entry)

XX

DE Humanised 3D6 heavy chain variable region #2.

Qy 121 YSGSSDYWGQGTTVTVSS 138
 |||||
 Db 121 YSGSSDYWGQGTTLVTVSS 138

RESULT 5

ABG74243

ID ABG74243 standard; protein; 133 AA.

XX

AC ABG74243;

XX

DT 22-APR-2003 (first entry)

XX

DE Mouse antibody 3D8 heavy chain variable region.

XX

KW T-cell receptor; cytostatic; dermatological; neuroprotective;

KW immunostimulant; GD3; ganglioside antigen; MB3.6; PSMA; tumour; 3D8; 4D4;

KW 3E11; prostate-specific membrane antigen; zeta signalling chain;

KW CD8alpha hinge; cancer; melanoma; neuroendocrine tumour; prostate cancer;

KW small cell lung cancer; heavy chain variable region; mouse.

XX

OS Mus sp.

XX

PN US2002132983-A1.

XX

PD 19-SEP-2002.

XX

PF 10-DEC-2001; 2001US-00006773.

XX

PR 30-NOV-2000; 2000US-0250087P.

PR 30-NOV-2000; 2000US-0250089P.

XX

PA (JUNG/) JUNGHANS R P.

XX

PI Junghans RP;

XX

DR WPI; 2003-208946/20.

DR N-PSDB; ABX16569.

XX

PT New chimeric molecule useful in treating patients with disorders, such as

PT melanoma, neuroendocrine disorders, prostate and small cell lung cancer

PT comprises GD3 and/or PSMA binding domains of antibody.

XX

PS Disclosure; Page 12; 35pp; English.

XX

CC The invention relates to a chimaeric molecule comprising the GD3

CC (ganglioside antigen) binding domain of antibody MB3.6, with any of 3

CC variable gene sequences, or the PSMA (prostate-specific membrane antigen)

CC binding domain of antibody 3D8, 4D4 and 3E11, with variable gene

CC sequences, the zeta signalling chain of the T cell receptor and an

CC intervening CD8alpha hinge in which cysteine residues have been mutated.

CC The chimaeric molecules expressed in T cells or NK cells or other

CC effector cells are useful in treating patients with cancers expressing

CC the GD3 (MB3.6 derivatives) or PSMA antigen (3D8, 4D4, 3E11 derivatives),

CC and/or together with each other or with heterologous constructs to engage

CC additional stimulatory and functional properties of the effector cells to


```

KW Crohn's disease; diabetes mellitus; antibody; mouse.
XX
OS Mus sp.
XX
PN WO2003037913-A2.
XX
PD 08-MAY-2003.
XX
PF 01-NOV-2002; 2002WO-US035333.
XX
PR 01-NOV-2001; 2001US-0346402P.
XX
PA (UABR-) UAB RES FOUND.
XX
PI Zhou T, Kimberly RP, Koopman WJ, Lobuglio AF, Buchsbaum DJ;
XX
DR WPI; 2003-441350/41.
DR N-PSDB; AAL60477.
XX
PT New purified antibody that specifically binds a TNF-related apoptosis-
PT inducing ligand receptor DR4 or DR5, useful for treating cancer,
PT inflammatory disease or autoimmune disease in a subject, e.g. asthma or
PT rheumatoid arthritis.
XX
PS Example 16; Page 224-225; 251pp; English.
XX
CC The invention relates to an antibody that specifically binds a tumour
CC necrosis factor (TNF)-related apoptosis-inducing ligand (TRAIL) receptor
CC DR4 or DR5. Antibodies of the invention are useful for selectively
CC inducing apoptosis in target cells expressing DR4, for inhibiting
CC proliferation of target cells expressing DR4 or for treating cancer,
CC inflammatory disease or autoimmune disease in a subject e.g. systemic
CC lupus erythematosus, Hashimoto's disease, rheumatoid arthritis, graft-
CC versus-host disease, Goodpasture's syndrome, Crohn's disease, multiple
CC sclerosis, diabetes mellitus, allergy, asthma, arteriosclerosis or
CC glomerular nephritis. The present sequence is mouse anti-human DR5
CC antibody (TRA-8) heavy chain
XX
SQ Sequence 462 AA;

Query Match 80.4%; Score 578; DB 6; Length 462;
Best Local Similarity 81.2%; Pred. No. 8.8e-44;
Matches 112; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

Qy 1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
Db 1 MNFGLSLIFLVLVLKGVQCEVMLLVESGGGLVKPGGSLKLSCAASGFTFSSYVMSWVRQTP 60

Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
Db 61 EKRLEWVATISSGGSYTYYPDSVKGRFTISRDNKNTLYLQMSSLRSEDAMYYCARRGD 120

Qy 121 YSGSSDYWGQGTTVTVSS 138
Db 121 SMITTDYWQGTTLTVSS 138

```

RESULT 8

AAU72801

ID AAU72801 standard; protein; 464 AA.

XX

AC AAU72801;

XX

DT 26-FEB-2002 (first entry)

XX

DE TRA-8 heavy chain.

XX

KW Tumour necrosis factor-related apoptosis-inducing ligand receptor; TRAIL;

KW TRAIL receptor DR5; cytostatic; apoptosis; cell proliferation;

KW autoimmune disease; systemic lupus erythematosus; Hashimoto's disease;

KW rheumatoid arthritis; Sjogren's syndrome; Chron's disease; anaemia;

KW Addison disease; scleroderma; Goodpasture's syndrome; sterility;

KW myasthenia gravis; multiple sclerosis; Basedow's disease; diabetes;

KW allergy; arteriosclerosis; myocarditis; cardiomyopathy;

KW glomerular nephritis; cancer; antibody; chromosome 8p21-22; TRA-8.

XX

OS Mus musculus.

XX

PN WO200183560-A1.

XX

PD 08-NOV-2001.

XX

PF 02-MAY-2001; 2001WO-US014151.

XX

PR 02-MAY-2000; 2000US-0201344P.

XX

PA (UABR-) UAB RES FOUND.

XX

PI Zhou T, Ichikawa K, Kimberly RP, Koopman WJ;

XX

DR WPI; 2002-049338/06.

DR N-PSDB; AAS97062.

XX

PT Novel antibody specific for tumor necrosis factor-related apoptosis-

PT inducing ligand, useful for inhibiting cell proliferation in cancer.

XX

PS Claim 26; Page 198-199; 229pp; English.

XX

CC The invention describes a novel antibody which recognizes a tumour

CC necrosis factor (TNF)-related apoptosis-inducing ligand (TRAIL) receptor

CC DR5 (located on chromosome 8p21-22). The antibody has apoptosis-inducing

CC activity to a cell expressing DR5 in vivo. It is also useful for

CC preparing a therapeutic for selective apoptosis of abnormal or

CC dysregulated cells, and for inhibiting cell proliferation in a cell,

CC preferably a human breast, ovary, colon, haematopoietic, prostate,

CC lymphatic, lung, glioma or liver cancer cell. A therapeutic agent may

CC also be administered e.g. paclitaxel, taxol or cycloheximide. The

CC antibody is used to treat an autoimmune disease, systemic lupus

CC erythematosus, Hashimoto's disease, rheumatoid arthritis, graft-versus-

CC host disease, Sjogren's syndrome, Chron's disease, pernicious anaemia,

CC Addison disease, scleroderma, Goodpasture's syndrome, autoimmune

CC haemolytic anaemia, sterility, myasthenia gravis, multiple sclerosis,

CC Basedow's disease, insulin-dependent diabetes mellitus, allergy, atopic

CC disease, arteriosclerosis, myocarditis, cardiomyopathy, glomerular

XX
PT Chimera antibody against drug resistant cancer - comprises variable
PT region homologous to region in mouse monoclonal antibody and constant
PT region homologous to region in human immunoglobulin.
XX
PS Disclosure; Fig 4; 20pp; Japanese.
XX
CC A chimeric antibody against drug-resistant cancer consists of (1) a
CC variable region having an amino acid sequence homologous to a variable
CC region in the mouse monoclonal antibody against drug- resistance and (2)
CC a constant region having an amino acid sequence homologous to the
CC constant region in human immunoglobulin. The chimeric antibody
CC selectively inhibits the growth of cancer cells showing drug resistance
CC or enhances the sensitivity to the drug. The antibody is very low in
CC immunogenicity. The MRK16-L chain is shown in AAQ20071. (Updated on 25-
CC MAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to standardise OS
CC field)
XX
SQ Sequence 138 AA;

Query Match 79.7%; Score 573; DB 2; Length 138;
Best Local Similarity 80.4%; Pred. No. 6.3e-44;
Matches 111; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

Qy 1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
| | | | | : | | | | | | | | | | | | | | | | | | | | | |
Db 1 MNFGLSLIFLVLILKGVQCEVILVESGGGLVKPGGSLKLSCAASGFTFSSYTMSWVRQTP 60

Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
: | | | | | : | | | | | | | | | | | | | | | | | | | | | |
Db 61 EKRLEWVATISSGGGNTYYPSVKGRFTISRDNAKNNLYLQMSSLRSEDTALYYCARYYR 120

Qy 121 YSGSSDYWGQGTTVTVSS 138
| | | | | | | | | | | | | | | | | | | | | |
Db 121 YEAWFASWGQGLVTVSA 138

RESULT 10

ABB79730

ID ABB79730 standard; protein; 144 AA.

XX

AC ABB79730;

XX

DT 29-OCT-2002 (first entry)

XX

DE Anti-Streptococcus mutans surface antigen MAb SWLA3 VH.

XX

KW Streptococcus mutans; monoclonal antibody; MAb; mouse; chimeric antibody;

KW antibody; anticaries; transgenic plant; transgenic animal; caries;

KW immunotherapy; therapy.

XX

OS Mus musculus.

XX

PN US2002068066-A1.

XX

PD 06-JUN-2002.

XX

PF 15-JUN-2001; 2001US-00881823.

XX

PR 20-AUG-1999; 99US-00378577.

XX

PA (SHIW/) SHI W.

PA (MORR/) MORRISON S L.

PA (TRIN/) TRINH K.

PA (WIMS/) WIMS L.

PA (CHEN/) CHEN L.

PA (ANDE/) ANDERSON M H.

XX

PI Shi W, Morrison SL, Trinh K, Wims L, Chen L, Anderson MH;

XX

DR WPI; 2002-565838/60.

DR N-PSDB; ABN84611.

XX

PT Treatment and prevention of dental caries in mammals, in particular

PT humans by orally administering genetically engineered or purified

PT antibodies that bind to surface antigens of carcinogenic organisms.

XX

PS Claim 14; Fig 3B; 30pp; English.

XX

CC The present sequence is the protein sequence of the heavy chain variable
CC region (VH) of the murine monoclonal antibody SWLA3 (IgG), which binds
CC specifically to the surface antigens of cariogenic type c Streptococcus
CC mutans (ATCC 25175). The monoclonal antibody is produced by SWLA3 (ATCC
CC HB 12558) hybridoma cells. In an example from the invention, chimeric
CC monoclonal antibody TEFÉ was produced comprising SWLA3 variable regions
CC and human antibody constant regions. Such chimeric monoclonal antibodies
CC can be used to prevent or treat dental caries in humans. The antibodies
CC engage the effector apparatus of the human immune system when they bind
CC cariogenic organisms, resulting in their destruction. The chimeric
CC antibodies may be produced in edible plants, in transgenic animals, or in
CC chicken eggs for oral ingestion

XX

SQ Sequence 144 AA;

Query Match 79.1%; Score 569; DB 5; Length 144;

Best Local Similarity 78.2%; Pred. No. 1.5e-43;

Matches 111; Conservative 11; Mismatches 16; Indels 4; Gaps 1;

Qy 1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
|:||||:|||| |||||:||||||| || |||||

Db 1 MDFGLSLVFLVLTCLKGVQCDVKLVESGGGLVNPGGSLKLSCAASGFTFSSYTMSWVRQTP 60

Qy 61 DKRLEWVASIRSGGGRYYSDNVKGRFTISRNAKNTLYLQMSSLKSEDTALYYCVR--- 117
:||||||| ||| ||| |:|||||||:|||||||:|||||||:||| |

Db 61 EKRLEWVASISSGGTYTYYPDSVKGRFTISRDNKNTLYLQMTSLKSEDTAMYYCSRDDG 120

Qy 118 -YDHYSGSSDYWGQGTTVTVSS 138
| | : |||||:|||||

Db 121 SYGSYYYAMDYWGQGTSTVTVSS 142

RESULT 11

AAR30480

ID AAR30480 standard; protein; 139 AA.

QY 121 Y-SGSSDYWGQGTTVTVSS 138
 | | : | | | | | : | | | |
 Db 120 YDSPAMDYWGQGTSVTVSS 138

RESULT 12

AAU76122

ID AAU76122 standard; protein; 140 AA.

XX

AC AAU76122;

XX

DT 08-MAY-2002 (first entry)

XX

DE Mouse monoclonal antibody 26-2F heavy chain variable region.

XX

KW Mouse; monoclonal antibody; heavy chain variable region; VH; angiogenin;

KW 26-2F; angiogenesis; tumour; cancer; retinopathy;

KW ocular neovascular disease; vitamin A deficiency; syphilis;

KW Kaposi's sarcoma; rheumatoid arthritis; macular degeneration;

KW sickle cell anaemia; Paget's disease; mycobacterial infection;

KW osteoarthritis; graft versus host disease; autoimmune disease;

KW type I diabetes; multiple sclerosis; systemic lupus erythematosus;

KW myasthenia gravis.

XX

OS Mus sp.

XX

FH Key Location/Qualifiers

FT Peptide 1. .19

FT /label= Signal_peptide

FT Protein 20. .140

FT /label= Mature_VH

FT Region 50. .54

FT /label= Complementarity_determining_region

FT /note= "This region is specifically claimed in claim 3"

FT Region 69. .85

FT /label= Complementarity_determining_region

FT /note= "This region is specifically claimed in claim 3"

FT Region 118. .129

FT /label= Complementarity_determining_region

FT /note= "This region is specifically claimed in claim 3"

XX

PN US2002010320-A1.

XX

PD 24-JAN-2002.

XX

PF 05-APR-1999; 99US-00286240.

XX

PR 05-APR-1999; 99US-00286240.

XX

PA (FETT/) FETT J W.

XX

PI Fett JW;

XX

DR WPI; 2002-187790/24.

DR N-PSDB; ABK15270.

XX

PT New antibody immunologically reactive to angiogenin useful for inhibiting
PT angiogenesis and for treating conditions associated with abnormal
PT angiogenesis e.g. cancer, ocular neovascular disease, rheumatoid
PT arthritis.

XX

PS Claim 6; Page 14; 20pp; English.

XX

CC The invention relates to an antibody immunologically reactive to
CC angiogenin or a fragment of angiogenin comprising light and heavy chain
CC nonhuman-derived complementarity determining regions having a binding
CC affinity to the angiogenin or its fragment in combination with human
CC derived polypeptide regions (e.g. mouse monoclonal antibody 26-2F). Also
CC included are an expression vector comprising a nucleic acid encoding the
CC antibody and a host cell transformed with the vector. The antibody or its
CC fragment is useful for inhibiting the angiogenic activity of angiogenin.
CC The antibody is useful for treating a tumour in humans, by inhibiting,
CC prohibiting, reducing or eliminating a tumour growth, or inhibiting the
CC ability of circulating tumour cell to form a vascularised tumour mass.
CC The antibody is useful for treating a mammal with abnormal or unwanted
CC angiogenesis, including cancer, and other diseases mediated by
CC angiogenesis, including ocular neovascular disease, diabetic retinopathy,
CC retinopathy of prematurity, corneal graft rejection, neovascular glaucoma
CC and retrolental fibroplasia, and other diseases associated with corneal
CC neovascularisation including epidemic keratoconjunctivitis, vitamin A
CC deficiency, contact lens overwear, atopic keratitis, superior limbic
CC keratitis, syphilis, mycobacteria infections, lipid degeneration,
CC chemical burns, bacterial ulcers, fungal ulcers, herpes simplex
CC infections, herpes zoster infections, protozoan infections, Kaposi's
CC sarcoma, Mooren ulcer, rheumatoid arthritis, polyarteritis, trauma,
CC Wegener's sarcoidosis, Scleritis, Steven Johnson's disease, and corneal
CC graft rejection. Diseases associated with retinal/choroidal
CC neovascularisation include macular degeneration, sickle cell anaemia,
CC sarcoid, Paget's disease, mycobacterial infections, Bechets disease,
CC trauma, osteoarthritis, Osler-Weber-Rendu disease, graft versus host
CC disease, transplant rejection, autoimmune diseases such as type I
CC diabetes, multiple sclerosis, systemic lupus erythematosus, and
CC myasthenia gravis. The present sequence is the heavy chain variable
CC region of mouse monoclonal antibody 26-2F

XX

SQ Sequence 140 AA;

Query Match 78.7%; Score 566; DB 5; Length 140;

Best Local Similarity 79.3%; Pred. No. 2.7e-43;

Matches 111; Conservative 13; Mismatches 14; Indels 2; Gaps 2;

Qy 1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
|:||||:||||:||||||| ||||||||| |||||||||:| |||||

Db 1 MDFGLSWVFLVLILKGVQCEVMLVESGGGLVKPGGSLKLSCAASGFTFSSYTMSWVRQTP 60

Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRANAKNTLYLQMSLKS EDTALYYCVRY-D 119
:|||||:| |||| || |:|||||||: |||||||||:||||||| | |

Db 61 EKRLEWVATISSGGGNTYYPDSVKGRFTISRDIANKNTLYLQMSLRSEDTALYYCTRLGD 120

Qy 120 H-YSGSSDYWGQGT TVTVSS 138

: |: : |||||||:|||||

Db 121 YGYAYTMDYWGQGT SVTVSS 140

RESULT 13

AAR27053

ID AAR27053 standard; protein; 139 AA.

XX

AC AAR27053;

XX

DT 01-MAR-1993 (first entry)

XX

DE Anti-CEA specific heavy chain variable region.

XX

KW Human; carcinoembryonic antigen; heavy chain; light chain; variable;
 KW region; diagnostic; tumour; markers; targetting.

XX

OS Mus musculus.

XX

FH Key Location/Qualifiers

FT Peptide 1. .19

FT /note= "signal peptide"

FT Protein 20. .139

FT /note= "mature peptide"

XX

PN JP04234987-A.

XX

PD 24-AUG-1992.

XX

PF 28-DEC-1990; 90JP-00408810.

XX

PR 28-DEC-1990; 90JP-00408810.

XX

PA (MITU) MITSUBISHI KASEI CORP.

XX

DR WPI; 1992-327631/40.

DR N-PSDB; AAQ28746.

XX

PT New DNA fragments encoding variable regions of ABS specific for human CEA
 PT - for diagnosing and monitoring tumours, as tumour markers and for
 PT treatment of tumours.

XX

PS Disclosure; Fig 1; 7pp; Japanese.

XX

CC The anti-CEA murine monoclonal antibody heavy chain variable region was
 CC obtd. by screening a cDNA library prepd. from mRNA obtd. from hybridomas
 CC producing anti-CEA-specific antibodies with a probe based on the constant
 CC region of the H-chain. The antibodies reacts specifically with human CEA
 CC and are useful as a diagnostic agents, as tumour markers for digestive
 CC organs, for diagnosis of malignant tumours; for monitoring after cancer
 CC operations, to follow up bloodless therapy or as therapeutic agents in
 CC passive immune therapy and targetting therapy. See also AAR27054

XX

SQ Sequence 139 AA;

Query Match 78.4%; Score 564; DB 2; Length 139;

Best Local Similarity 79.9%; Pred. No. 4.1e-43;

Matches 111; Conservative 11; Mismatches 15; Indels 2; Gaps 2;

Qy 1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60

PT angiogenesis and for treating conditions associated with abnormal
PT angiogenesis e.g. cancer, ocular neovascular disease, rheumatoid
PT arthritis.

XX

PS Claim 11; Page; 20pp; English.

XX

CC The invention relates to an antibody immunologically reactive to
CC angiogenin or a fragment of angiogenin comprising light and heavy chain
CC nonhuman-derived complementarity determining regions having a binding
CC affinity to the angiogenin or its fragment in combination with human
CC derived polypeptide regions (e.g. mouse monoclonal antibody 26-2F). Also
CC included are an expression vector comprising a nucleic acid encoding the
CC antibody and a host cell transformed with the vector. The antibody or its
CC fragment is useful for inhibiting the angiogenic activity of angiogenin.
CC The antibody is useful for treating a tumour in humans, by inhibiting,
CC prohibiting, reducing or eliminating a tumour growth, or inhibiting the
CC ability of circulating tumour cell to form a vascularised tumour mass.
CC The antibody is useful for treating a mammal with abnormal or unwanted
CC angiogenesis, including cancer, and other diseases mediated by
CC angiogenesis, including ocular neovascular disease, diabetic retinopathy,
CC retinopathy of prematurity, corneal graft rejection, neovascular glaucoma
CC and retrolental fibroplasia, and other diseases associated with corneal
CC neovascularisation including epidemic keratoconjunctivitis, vitamin A
CC deficiency, contact lens overwear, atopic keratitis, superior limbic
CC keratitis, syphilis, mycobacteria infections, lipid degeneration,
CC chemical burns, bacterial ulcers, fungal ulcers, herpes simplex
CC infections, herpes zoster infections, protozoan infections, Kaposi's
CC sarcoma, Mooren ulcer, rheumatoid arthritis, polyarteritis, trauma,
CC Wegener's sarcoidosis, Scleritis, Steven Johnson's disease, and corneal
CC graft rejection. Diseases associated with retinal/choroidal
CC neovascularisation include macular degeneration, sickle cell anaemia,
CC sarcoid, Paget's disease, mycobacterial infections, Bechets disease,
CC trauma, osteoarthritis, Osler-Weber-Rendu disease, graft versus host
CC disease, transplant rejection, autoimmune diseases such as type I
CC diabetes, multiple sclerosis, systemic lupus erythematosus, and
CC myasthenia gravis. The present sequence represents the E59Y mutant of the
CC mouse monoclonal antibody 26-2F light chain variable region. Note: The
CC present sequence is not shown in the specification but was created by the
CC indexer using the sequence appearing as AAU76122 and the information in
CC the claims

XX

SQ Sequence 140 AA;

Query Match 78.4%; Score 564; DB 5; Length 140;

Best Local Similarity 79.3%; Pred. No. 4.2e-43;

Matches 111; Conservative 13; Mismatches 14; Indels 2; Gaps 2;

Qy 1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
|:||||:||||:||||||| ||||||||| |||||||||:| |||||

Db 1 MDFGLSWVFLVLILKGVQCEVMLVESGGGLVKPGGSLKLSCAASGFTFSYTMSSWVRQYP 60

Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRANAKNTLYLQMSSLKSEDTALYYCVRY-D 119
:||||||:| ||| |||:|||||||: |||||||||:||||||| | |

Db 61 EKRLEWVATISSGGGNTYYPSVKGRFTISRDIKNTLYLQMSSLRSEDTALYYCTRLGD 120

Qy 120 H-YSGSSDYWGQGTTVTVSS 138
: |: : |||||:|||||

Db 121 YGYAYTMDYWGQGTSTVTVSS 140

RESULT 15

AAW03722

ID AAW03722 standard; protein; 138 AA.

XX

AC AAW03722;

XX

DT 02-APR-1997 (first entry)

XX

DE Anti-human gp39 MAb 39-1.106 heavy chain variable region.

XX

KW Heavy chain; variable region; murine; mouse; anti-human; disease;

KW glycoprotein 39; gp39; monoclonal; antibody; 39-1.106; hybridoma;

KW diagnosis; inhibition; B-cell; activation; treatment; disorder; immune;

KW autoimmune; allergic response; organ rejection; drug; graft versus host;

KW cell imaging; tumour; targetted; delivery; targeted.

XX

OS Mus musculus.

XX

FH Key Location/Qualifiers

FT Peptide 1. .19

FT /label= sig_peptide

FT Peptide 20. .138

FT /label= mat_peptide

FT Region 50. .54

FT /note= "complementarity determining region 1"

FT Region 69. .84

FT /note= "complementarity determining region 2"

FT Region 117. .126

FT /note= "complementarity determining region 3"

XX

PN WO9623071-A2.

XX

PD 01-AUG-1996.

XX

PF 26-JAN-1996; 96WO-US001119.

XX

PR 26-JAN-1995; 95US-00379057.

XX

PA (BRIM) BRISTOL-MYERS SQUIBB CO.

XX

PI Siadak A, Hollenbaugh D, Gilliland LK, Gordon ML, Bajorath J;

PI Aruffo AA, Harris LJ;

XX

DR WPI; 1996-362694/36.

DR N-PSDB; AAT35974.

XX

PT Monoclonal antibodies specific for different epitope(s) on human gp39 -

PT used for inhibiting B cell activation and for the diagnosis of various

PT disorders, e.g. cancer, psoriasis etc. .

XX

PS Claim 91; Fig 6B; 167pp; English.

XX

CC The present sequence is the heavy chain variable region of the murine

CC anti-human glycoprotein (gp) 39 monoclonal antibody (MAb) 39-1.106 (a

CC member of the murine III(D) subgroup). The MAb was prepd. by immunising a
 CC 6-8 week old BALB/c mouse with a gp39-CD8 fusion protein, and 3 days
 CC later harvesting and fusing spleen and lymph cells to mouse melanoma
 CC cells, to produce an anti-human gp39 MAb producing hybridoma. The MAb may
 CC be useful for diagnosing disease states, inhibiting B-cell activation and
 CC for treating immunological disorders, e.g. autoimmune disorders, allergic
 CC responses, organ rejection and graft versus host disease. It may also be
 CC used for imaging cells which express gp39 on their surface, e.g. tumour
 CC cells, and to target therapeutic agents to such cells. The MAb inhibits
 CC the CD40/gp39 interaction, therefore limiting both prim. and sec.
 CC responses to T-cell dependent antigens and Ab prodn. specific to these
 CC antigens. A typical compsn. for intramuscular injection pref. contains 50
 CC mg of MAb in 1 ml of sterile buffered water

XX

SQ Sequence 138 AA;

Query Match 78.3%; Score 563; DB 2; Length 138;

Best Local Similarity 79.1%; Pred. No. 5e-43;

Matches 110; Conservative 11; Mismatches 16; Indels 2; Gaps 2;

Qy 1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
 ||||| ||||||||||||||||||||||||||||||| ||||| |||||:| |||||

Db 1 MNFGFSLIFLVLVLKGVQCEVKLVESGGGLVKPGGSLKLSCCTTS GFTFN NYAMS WVRQTP 60

Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISR ENAKNTLYLQMSSLKSEDTALYYCVR-YD 119
 :||||||| | | ||| |:|:||||||:|:| |||||||:||||:| | |

Db 61 EKRLWVASI-SSGDSTYYPD SVRGRFTISRDNARNILY LQMSSLRSEDTAMYYCARHYD 119

Qy 120 HYSGSSDYWGQGT TVTVSS 138
 : | : |||||||:|||||

Db 120 YDSYAMDYWGQGT SVTVSS 138

Search completed: May 17, 2004, 11:30:35

Job time : 54.6444 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 17, 2004, 11:29:03 ; Search time 16.8667 Seconds
(without alignments)
422.394 Million cell updates/sec

Title: US-10-010-942B-4
Perfect score: 719
Sequence: 1 MNFGLSLIFLVVLKGVQCE.....DHYSGSSDYWGQGTTTVTVSS 138

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%						
Result		Query						
No.	Score	Match	Length	DB	ID		Description	
1	566.5	78.8	135	3	US-08-579-378A-16		Sequence 16, Appl	
2	563	78.3	138	2	US-08-379-057-14		Sequence 14, Appl	
3	551	76.6	158	2	US-08-653-402B-6		Sequence 6, Appli	
4	549	76.4	140	3	US-08-836-561-23		Sequence 23, Appl	
5	549	76.4	140	4	US-09-434-122-23		Sequence 23, Appl	
6	549	76.4	247	5	PCT-US94-07659-2		Sequence 2, Appli	
7	545.5	75.9	135	3	US-08-579-378A-20		Sequence 20, Appl	
8	541	75.2	136	4	US-08-976-183A-33		Sequence 33, Appl	
9	540	75.1	136	4	US-08-976-183A-31		Sequence 31, Appl	
10	537	74.7	136	4	US-08-976-183A-32		Sequence 32, Appl	
11	536	74.5	136	4	US-08-976-183A-34		Sequence 34, Appl	

12	535	74.4	136	1	US-08-253-877C-57	Sequence 57, Appl
13	535	74.4	136	2	US-08-452-164A-57	Sequence 57, Appl
14	535	74.4	138	1	US-08-053-171-7	Sequence 7, Appli
15	535	74.4	138	1	US-08-053-171-11	Sequence 11, Appl
16	535	74.4	158	2	US-08-653-402B-10	Sequence 10, Appl
17	514.5	71.6	139	1	US-08-129-930B-96	Sequence 96, Appl
18	514.5	71.6	139	3	US-08-134-346A-51	Sequence 51, Appl
19	514.5	71.6	139	4	US-08-976-288A-96	Sequence 96, Appl
20	513	71.3	170	2	US-08-652-558-40	Sequence 40, Appl
21	512.5	71.3	159	2	US-08-653-402B-2	Sequence 2, Appli
22	497.5	69.2	255	2	US-07-690-192-4	Sequence 4, Appli
23	494.5	68.8	463	4	US-09-472-087-1	Sequence 1, Appli
24	494.5	68.8	463	4	US-09-472-087-63	Sequence 63, Appl
25	494.5	68.8	463	4	US-09-472-087-64	Sequence 64, Appl
26	493	68.6	464	4	US-09-472-087-2	Sequence 2, Appli
27	493	68.6	464	4	US-09-472-087-66	Sequence 66, Appl
28	490.5	68.2	135	5	PCT-US95-07302-8	Sequence 8, Appli
29	486	67.6	130	4	US-09-225-322B-8	Sequence 8, Appli
30	486	67.6	130	4	US-09-764-304-8	Sequence 8, Appli
31	484.5	67.4	122	1	US-07-634-278-48	Sequence 48, Appl
32	484.5	67.4	122	1	US-08-477-728-48	Sequence 48, Appl
33	484.5	67.4	122	1	US-08-474-040-48	Sequence 48, Appl
34	484.5	67.4	122	1	US-08-487-200-48	Sequence 48, Appl
35	484.5	67.4	122	3	US-08-484-537-48	Sequence 48, Appl
36	484	67.3	130	4	US-09-225-322B-18	Sequence 18, Appl
37	484	67.3	130	4	US-09-764-304-18	Sequence 18, Appl
38	482.5	67.1	135	3	US-08-619-491-8	Sequence 8, Appli
39	482.5	67.1	463	4	US-09-472-087-4	Sequence 4, Appli
40	482.5	67.1	463	4	US-09-472-087-68	Sequence 68, Appl
41	480.5	66.8	456	4	US-09-495-880A-11	Sequence 11, Appl
42	478.5	66.6	135	3	US-08-619-491-4	Sequence 4, Appli
43	478.5	66.6	135	5	PCT-US95-07302-4	Sequence 4, Appli
44	477	66.3	239	2	US-08-553-497A-18	Sequence 18, Appl
45	475	66.1	123	4	US-09-344-587-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1

US-08-579-378A-16

; Sequence 16, Application US/08579378A

; Patent No. 6210671

; GENERAL INFORMATION:

; APPLICANT: Co, Man Sung

; TITLE OF INVENTION: Humanized Antibodies Reactive with

; TITLE OF INVENTION: L-Selectin

; NUMBER OF SEQUENCES: 20

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew

; STREET: One Market Plaza, Steuart Tower, Suite 2000

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94105

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

RESULT 3

US-08-653-402B-6

; Sequence 6, Application US/08653402B

; Patent No. 5969107

; GENERAL INFORMATION:

; APPLICANT: CARCELLER, Ana

; APPLICANT: ROSELL, Elisabet

; APPLICANT: GOMEZ, Alicia

; APPLICANT: ADEN, Jaume

; APPLICANT: PIULATS, Jaume

; TITLE OF INVENTION: Anti-idiotypic antibodies which induce an

; TITLE OF INVENTION: immune response against epidermal growth factor

receptor.

; NUMBER OF SEQUENCES: 13

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Millen, White, Zelano & Branigan, P.C.

; STREET: 2200 Clarendon Boulevard, Suite 1400

; CITY: Arlington

; STATE: Virginia

; COUNTRY: U.S.A.

; ZIP: 22201

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/653,402B

; FILING DATE: 24-MAY-1996

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: EP 95107967.2

; FILING DATE: 26-MAY-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Lebovitz, Richard M.

; REGISTRATION NUMBER: 37,067

; REFERENCE/DOCKET NUMBER: MERCK 1781

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 703-243-6333

; TELEFAX: 703-243-6410

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 158 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-653-402B-6

Query Match 76.6%; Score 551; DB 2; Length 158;

Best Local Similarity 77.8%; Pred. No. 5.9e-51;

Matches 112; Conservative 9; Mismatches 17; Indels 6; Gaps 2;

Qy 1 MNFGLSLIFLVLVKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60

|:||||||||| || |:||||||||| | ||||||||||| |||||

Db 1 MDFGLSLIFLVLVFKGVLCVVKLVESGGGLVKLGSLKLSCAASGFTFSNYMSWVRQTP 60

; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-836-561-23

Query Match 76.4%; Score 549; DB 3; Length 140;
Best Local Similarity 74.3%; Pred. No. 8.3e-51;
Matches 104; Conservative 16; Mismatches 18; Indels 2; Gaps 1;

Qy 1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
| | | | | | | | | | : | | | | | | : | | | | | | | | | | : | | : | | |
Db 1 MNFGLSLIFLALILKGVQCEVQLVESGGDLVKPGSLKLSCAASGFTFSQYGMWIRQIS 60

Qy 61 DKRLEWVASIRSGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
| | | | | | : | | | : | : | | | | : | : | | | | | | : | | | | | |
Db 61 DKRPEWVAIAISSGGSYIHFPDSLKGRFTVSRDNAKNTLYLEMSGLKSEDTAMYYCARRGF 120

Qy 121 YSG--SSDYWGQGTTVTVSS 138
| : | | | | | : | | | |
Db 121 YGNYRAMDYWGQGTTSVTVSS 140

RESULT 5

US-09-434-122-23

; Sequence 23, Application US/09434122
; Patent No. 6538111

; GENERAL INFORMATION:

; APPLICANT: KOIKE, Masamichi
; FURUYA, Akiko
; NAKAMURA, Kazuyasu
; IIDA, Akihiro
; ANAZAWA, Hideharu
; HANAI, No. 6538111uo
; TAKATSU, Kiyoshi

; TITLE OF INVENTION: Antibody Against Human Interleukin-5
; Receptor Alpha Chain

; NUMBER OF SEQUENCES: 106

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/434,122
; FILING DATE: 05-May-1999

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/836,561
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: JP 232384/95
; FILING DATE: 11-SEP-1995

```

; ATTORNEY/AGENT INFORMATION:
; NAME: Lawrence, III, Stanton T
; REGISTRATION NUMBER: 25,736
; REFERENCE/DOCKET NUMBER: 7005-115-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 140 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-434-122-23

```

```

Query Match          76.4%; Score 549; DB 4; Length 140;
Best Local Similarity 74.3%; Pred. No. 8.3e-51;
Matches 104; Conservative 16; Mismatches 18; Indels 2; Gaps 1;

```

```

Qy      1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKGASLKLSCAASGFTFSNYGMSWVRQNS 60
      |||||:|:|||||:||||| ||||| |||||:|:|:|
Db      1 MNFGLSLIFLALILKGVQCEVQLVESGGDLVKGPGSLKLSCAASGFTFSNYGMAWIRQIS 60

Qy      61 DKRLEWVASIRSGGRTYYSDNVKGRFTISRENAKNTLYLQMSLKSSEDALYYCVRYDH 120
      ||| |||:| ||| :|:|:|:|:|:|:| |||||:| |||||:| |||
Db      61 DKRPEWVAIAISSGGSYIHFPDSLKGRFTVSRDNAKNTLYLEMSGLKSEDTAMYYCARRGF 120

Qy      121 YSG--SSDYWGQGTTVTVSS 138
      | : |||||:|||||
Db      121 YGNRYAMDYWGQGTSTVTVSS 140

```

RESULT 6

PCT-US94-07659-2

; Sequence 2, Application PC/TUS9407659

; GENERAL INFORMATION:

```

; APPLICANT: Young, Peter
; APPLICANT: Gross, Mitchell
; APPLICANT: Jonak, Zdenka L.
; APPLICANT: Theisen, Timothy
; APPLICANT: Hurle, Mark
; APPLICANT: Jackson, Jeffrey R.
; TITLE OF INVENTION: Recombinant and Humanized Il-1 beta
; TITLE OF INVENTION: Antibodies for Treatment of Il-1 Mediated Inflammatory
; TITLE OF INVENTION: Disorders in Man
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation - Corp.
; ADDRESSEE: Intellectual Property
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA

```

```

; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07659
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/090,534
; FILING DATE: 09-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50171-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 270-5024
; TELEFAX: (610) 270-5090
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 247 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US94-07659-2

```

```

Query Match          76.4%; Score 549; DB 5; Length 247;
Best Local Similarity 78.3%; Pred. No. 1.7e-50;
Matches 108; Conservative 7; Mismatches 23; Indels 0; Gaps 0;

```

```

Qy      1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
        ||||| ||||| ||||:|| ||||| ||||| ||||| ||||| ||||| |||||
Db      1 MNFGLRLIFLVLTLLKGVKCEVHLVESGGGLVKPGGSLKLSCAASGFAFSSYDMSWVRQTP 60

Qy      61 DKRLEWVASIRSGGGRITYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
        :|||:||| | ||| ||| | ||||| ||||| ||||| ||||| ||||| |||||
Db      61 EKRLDWVAYISSGGGGTYYPDTVKGRTISRDNKNTLYLQMSSLKSEDTAMYHCARGGV 120

Qy      121 YSGSSDYWGQGTTVTVSS 138
        | | | | |||||
Db      121 RRGYFDVWGAGTTTVTVSS 138

```

```

RESULT 7
US-08-579-378A-20
; Sequence 20, Application US/08579378A
; Patent No. 6210671
; GENERAL INFORMATION:
; APPLICANT: Co, Man Sung
; TITLE OF INVENTION: Humanized Antibodies Reactive with
; TITLE OF INVENTION: L-Selectin
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One MarketPlaza, Steuart Tower, Suite 2000

```

```

; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/579,378A
; FILING DATE: 27-DEC-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/160,074
; FILING DATE: 30-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/983,946
; FILING DATE: 01-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95112895.8
; FILING DATE: 17-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95114696.8
; FILING DATE: 19-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschutz, Joe O.
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 11823-002220
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 135 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-579-378A-20

```

```

Query Match          75.9%; Score 545.5; DB 3; Length 135;
Best Local Similarity 79.0%; Pred. No. 1.9e-50;
Matches 109; Conservative 9; Mismatches 17; Indels 3; Gaps 2;

```

```

Qy      1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1 MNFGSSLIFLVVLKGVQCEVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMSWVRQAP 60

Qy     61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
      | ||||| | || ||| |: ||||| |: ||||| |: |||: |||: |||
Db     61 GKGLEWVASI-STGGSTYYPDSVKGRFTISRDNAKNTLYLQMNSLRAEDTAVYYCAR--D 117

Qy    121 YSGSSDYWGQGT TVTVSS 138
      | | ||||| |||||
Db    118 YDGYFDYWGQGT LVTVSS 135

```

RESULT 8

US-08-976-183A-33

```
; Sequence 33, Application US/08976183A
; Patent No. 6307026
; GENERAL INFORMATION:
;   APPLICANT: King, David J.
;   APPLICANT: Adair, John R.
;   APPLICANT: Owens, Raymond J.
;   TITLE OF INVENTION: HUMANISED ANTIBODIES DIRECTED AGAINST A33
;   TITLE OF INVENTION: ANTIGEN
;   NUMBER OF SEQUENCES: 55
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: FOLEY & LARDNER
;     STREET: 3000 K. Street, N.W., Suite 500
;     CITY: Washington, D.C.
;     COUNTRY: USA
;     ZIP: 20007
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/976,183A
;     FILING DATE:
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US/08/595,848
;     FILING DATE: 02-FEB-1996
;     APPLICATION NUMBER: PCT/GB93/02529
;     FILING DATE: 10-DEC-1993
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: GB 9225853.2
;     FILING DATE: 10-DEC-1993
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: 9315249.4
;     FILING DATE: 22-JUL-1993
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Bernhard D. Saxe
;     REGISTRATION NUMBER: 28,665
;     REFERENCE/DOCKET NUMBER: 40283/151/CARA
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (202) 672-5300
;     TELEFAX: (202) 672-5399
;     TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 33:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 136 amino acids
;       TYPE: amino acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;     MOLECULE TYPE: protein
US-08-976-183A-33
```

```
Query Match          75.2%;  Score 541;  DB 4;  Length 136;
Best Local Similarity 75.5%;  Pred. No. 5.7e-50;
Matches 108;  Conservative 10;  Mismatches 13;  Indels 12;  Gaps 2;
```

Qy 1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
 |||||:||||| ||||| |||||
 Db 1 MNFGLSLIFLVLILKGVQCEVKLVESGGGLVKPGGSLKLSCAASGFAFSTYDMSWVRQTP 60
 Qy 61 DKRLEWVASIRSGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYC----- 115
 :|||||:| ||| ||| |:|||||:|:|:|||||:|||||
 Db 61 EKRLEWVATISSGGSYTYLDSVKGRFTISRDSARNTLYLQMSSLRSEDTALYYCAPTTV 120
 Qy 116 VRYDHYSGSSDYWGQTTTVTVSS 138
 | : ||||| |||||
 Db 121 VPF-----AYWGQTLTVTVSA 136

RESULT 9

US-08-976-183A-31

; Sequence 31, Application US/08976183A

; Patent No. 6307026

; GENERAL INFORMATION:

; APPLICANT: King, David J.

; APPLICANT: Adair, John R.

; APPLICANT: Owens, Raymond J.

; TITLE OF INVENTION: HUMANISED ANTIBODIES DIRECTED AGAINST A33

; TITLE OF INVENTION: ANTIGEN

; NUMBER OF SEQUENCES: 55

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: FOLEY & LARDNER

; STREET: 3000 K. Street, N.W., Suite 500

; CITY: Washington, D.C.

; COUNTRY: USA

; ZIP: 20007

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/976,183A

; FILING DATE:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/595,848

; FILING DATE: 02-FEB-1996

; APPLICATION NUMBER: PCT/GB93/02529

; FILING DATE: 10-DEC-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: GB 9225853.2

; FILING DATE: 10-DEC-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 9315249.4

; FILING DATE: 22-JUL-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Bernhard D. Saxe

; REGISTRATION NUMBER: 28,665

; REFERENCE/DOCKET NUMBER: 40283/151/CARA

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 672-5300

; TELEFAX: (202) 672-5399

; TELEX: 904136

```
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 136 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-976-183A-31
```

```
Query Match          75.1%; Score 540; DB 4; Length 136;
Best Local Similarity 74.8%; Pred. No. 7.2e-50;
Matches 107; Conservative 11; Mismatches 13; Indels 12; Gaps 2;
```

```
Qy      1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
      |||||:||||:||||||||||||||||||| ||||| || |||||
Db      1 MNFGLSLVFLVLILKGVQCEVKLVESGGGLVKPGGSLKLSCAASGFAFSTYDMSWVRQTP 60

Qy     61 DKRLEWVASIRSGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYC----- 115
      :|||||:| ||| |||.:|||||||:|:|:|||||||:|||||||
Db     61 EKRLEWVATISSGGSYTYLDSVKGRFTISRDSARNTLYLQMSSLRSEDTALYYCAPTTV 120

Qy    116 VRYDHYSGSSDYWGQGTTVTVSS 138
      | :      ||||| ||||:
Db    121 VPF-----AYWGQGTTLVTVSA 136
```

RESULT 10

US-08-976-183A-32

```
; Sequence 32, Application US/08976183A
; Patent No. 6307026
; GENERAL INFORMATION:
;   APPLICANT: King, David J.
;   APPLICANT: Adair, John R.
;   APPLICANT: Owens, Raymond J.
;   TITLE OF INVENTION: HUMANISED ANTIBODIES DIRECTED AGAINST A33
;   TITLE OF INVENTION: ANTIGEN
;   NUMBER OF SEQUENCES: 55
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: FOLEY & LARDNER
;     STREET: 3000 K. Street, N.W., Suite 500
;     CITY: Washington, D.C.
;     COUNTRY: USA
;     ZIP: 20007
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/976,183A
;     FILING DATE:
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US/08/595,848
;     FILING DATE: 02-FEB-1996
;     APPLICATION NUMBER: PCT/GB93/02529
;     FILING DATE: 10-DEC-1993
;   PRIOR APPLICATION DATA:
```

```

; APPLICATION NUMBER: GB 9225853.2
; FILING DATE: 10-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9315249.4
; FILING DATE: 22-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Bernhard D. Saxe
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 40283/151/CARA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 136 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-976-183A-32

```

```

Query Match          74.7%; Score 537; DB 4; Length 136;
Best Local Similarity 74.8%; Pred. No. 1.5e-49;
Matches 107; Conservative 10; Mismatches 14; Indels 12; Gaps 2;

```

```

Qy      1 MNFGSLIFLVLVKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
      ||||| |||||:||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1 MNFGFSLIFLVLILKGVQCEVKLVESGGGLVKPGGSLKLSCAASGFAFSTYDMSWVRQTP 60

Qy      61 DKRLEWVASIRSGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYC----- 115
      :|||||:| ||| ||| |:|||||:|:|:|||||:|:|:|||||:|:|:|||||
Db      61 EKRLEWVATISSGGSYTYLDSVKGRFTISRDSARNTLYLQMSSLRSEDALYYCAPTTV 120

Qy      116 VRYDHYSGSSDYWGQGTTVTVSS 138
      | : ||||| ||||:
Db      121 VPF-----AYWGQGTTLTVSA 136

```

RESULT 11

US-08-976-183A-34

; Sequence 34, Application US/08976183A

; Patent No. 6307026

; GENERAL INFORMATION:

```

; APPLICANT: King, David J.
; APPLICANT: Adair, John R.
; APPLICANT: Owens, Raymond J.
; TITLE OF INVENTION: HUMANISED ANTIBODIES DIRECTED AGAINST A33
; TITLE OF INVENTION: ANTIGEN
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K. Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:

```


; APPLICANT: Hamann, Philip R.
 ; APPLICANT: Hinman, Lois
 ; APPLICANT: Hollander, Irwin
 ; APPLICANT: Holcomb, Ryan
 ; APPLICANT: Hallett, William
 ; APPLICANT: Tsou, Hwei-Ru
 ; APPLICANT: Weiss, Martin J.
 ; TITLE OF INVENTION: Conjugates of Methyltrithio Antitumor
 ; TITLE OF INVENTION: Agents and Intermediates for Their Synthesis
 ; NUMBER OF SEQUENCES: 73
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: American Cyanamid Company
 ; STREET: One Cyanamid Plaza
 ; CITY: Wayne
 ; STATE: New Jersey
 ; COUNTRY: U.S.A.
 ; ZIP: 07470-8426
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/253,877C
 ; FILING DATE: 03-JUN-1994
 ; CLASSIFICATION: 424
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Barnhard, Elizabeth M.
 ; REGISTRATION NUMBER: 31,088
 ; REFERENCE/DOCKET NUMBER: 32,368
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 201-831-3246
 ; TELEFAX: 201-331-3305
 ; INFORMATION FOR SEQ ID NO: 57:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 136 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-08-253-877C-57

Query Match 74.4%; Score 535; DB 1; Length 136;
 Best Local Similarity 74.1%; Pred. No. 2.5e-49;
 Matches 106; Conservative 11; Mismatches 14; Indels 12; Gaps 2;

Qy 1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
 |||||:||||:||||| ||||| ||||| |||||
 Db 1 MNFGLSLVFLVLILKGVQCEVKLVESGGGLVKPGGSLKLSCAASGFAFSTYDMSWVRQTP 60
 Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYC----- 115
 :|||||:| ||| ||| |:|||||::: :|||||:|||||
 Db 61 EKRLEWVATISSGGSYTYLDVSKGRFTISRDSRPNTLYLQMSSLRSEDTALYYCAPTTV 120
 Qy 116 VRYDHYSGSSDYWGQGTTVTVSS 138
 | : ||||| |||||
 Db 121 VPF-----AYWGQGTTLTVSA 136

US-08-452-164A-57

US-03-452-164A-57

```
Qy      1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKGPGASLKLSCAASGFTFSNYGMSWVRQNS   60
        |||||::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1 MNFGLSLVFLVLILKGVQCEVKLVESGGGLVKGPGGSLKLSCAASGFAPSTYDMSWVRQTP   60

Qy     61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYC----- 115
        :|||::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```


Qy 121 YSGSSDYWGQGTTVTVSS 138
| | | | | | | | :
Db 121 YGAWFAYWGQGTTLVTVSA 138

RESULT 15

US-08-053-171-11

; Sequence 11, Application US/08053171
; Patent No. 5562903
; GENERAL INFORMATION:
; APPLICANT: Co, Loibner
; TITLE OF INVENTION: Antibody Derivatives
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/053,171
; FILING DATE: 22-APR-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, Willaim M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-54-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 138 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-053-171-11

Query Match 74.4%; Score 535; DB 1; Length 138;
Best Local Similarity 75.4%; Pred. No. 2.5e-49;
Matches 104; Conservative 12; Mismatches 22; Indels 0; Gaps 0;

Qy 1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
| | | | | | | | | | | | | | | | | | : | | | | | | | | : | | | |
Db 1 MNLGLSLIFLVVLKGVQCEVKLVESGGGLVQPGGSLKLSCATSGFTFSDYYMYWVRQTP 60

Qy 61 DKRLEWVASIRSGGGRITYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
: | | | | | | : | | : | | : | | | | | | : | | | | : | | | |
Db 61 EKRLEWVAYISNGGSSHYVDSVKGRFTISRDNKNTLYLQMSRLRSEDAMYHCARGMD 120

Qy 121 YSGSSDYWGQGTTVTVSS 138
| ||||| ||||:
Db 121 YGAWFAYWGQGTTLVTVSA 138

Search completed: May 17, 2004, 11:33:54
Job time : 16.8667 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 17, 2004, 11:25:03 ; Search time 13.8 Seconds
(without alignments)
961.915 Million cell updates/sec

Title: US-10-010-942B-4
Perfect score: 719
Sequence: 1 MNFGLSLIFLVLVLKGVQCE.....DHYSGSSDYWGQTTVTVSS 138

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query		DB	ID	Description
	Score	Match Length			
1	573	79.7	138	2	S09258 Ig heavy chain V r
2	569	79.1	152	2	B26471 Ig heavy chain pre
3	559.5	77.8	139	2	S38808 Ig heavy chain - m
4	544	75.7	142	2	C34903 Ig heavy chain pre
5	521.5	72.5	140	2	S70442 Ig heavy chain pre
6	517	71.9	140	2	S31686 Ig heavy chain V r
7	516	71.8	160	2	S05271 Ig heavy chain pre
8	514	71.5	134	2	S31699 Ig heavy chain V r
9	513	71.3	140	2	S31588 Ig heavy chain V r
10	512	71.2	117	1	HVMS84 Ig heavy chain pre
11	510	70.9	117	1	HVMS34 Ig heavy chain pre
12	508	70.7	136	2	S31615 hypothetical prote
13	504	70.1	140	2	S22657 Ig heavy chain pre

14	502.5	69.9	136	1	G1MS21	Ig heavy chain pre
15	502	69.8	138	2	S31666	Ig heavy chain V r
16	501	69.7	117	1	HVMS39	Ig heavy chain pre
17	495	68.8	135	2	S31598	Ig heavy chain V r
18	493	68.6	134	2	S31679	Ig heavy chain V r
19	492.5	68.5	141	2	S31669	Ig heavy chain V r
20	492	68.4	117	1	HVMSRF	Ig heavy chain pre
21	492	68.4	139	2	I37781	Ig variable region
22	490	68.2	122	2	E27888	Ig heavy chain V r
23	487.5	67.8	119	2	F27888	Ig heavy chain V r
24	485.5	67.5	136	2	S31587	Ig heavy chain V r
25	484.5	67.4	151	2	A60943	Ig heavy chain pre
26	484	67.3	117	1	HVMS57	Ig heavy chain pre
27	484	67.3	140	2	A30532	Ig heavy chain pre
28	483	67.2	120	2	S55536	Ig heavy chain V r
29	481.5	67.0	147	2	I37780	Ig variable region
30	480.5	66.8	118	2	PH0096	Ig heavy chain V r
31	480.5	66.8	121	2	S55540	Ig heavy chain V r
32	480.5	66.8	254	2	B31790	Ig heavy chain V r
33	479	66.6	120	2	S55538	Ig heavy chain V r
34	479	66.6	120	2	S55539	Ig heavy chain V r
35	477.5	66.4	121	2	H27888	Ig heavy chain V r
36	477.5	66.4	137	2	S31701	Ig heavy chain V r
37	477.5	66.4	139	2	S31674	Ig heavy chain V r
38	476.5	66.3	137	2	S78054	Ig heavy chain pre
39	476	66.2	120	2	S55537	Ig heavy chain V r
40	473.5	65.9	118	2	PH0097	Ig heavy chain V r
41	472	65.6	132	2	S31603	Ig heavy chain V r
42	471	65.5	130	2	PL0098	Ig heavy chain pre
43	469	65.2	118	2	S20641	Ig heavy chain V r
44	467.5	65.0	135	2	I37778	Ig variable region
45	467.5	65.0	145	2	S11239	Ig heavy chain V r

ALIGNMENTS

RESULT 1

S09258

Ig heavy chain V region precursor - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 23-Jul-1999

C;Accession: S09258

R;Hamada, H.; Maezawa, K.; Tsuruo, T.

Nucleic Acids Res. 18, 1900, 1990

A;Title: Nucleotide sequences of the variable regions of a mouse monoclonal antibody MRK16.

A;Reference number: S09258; MUID:90245594; PMID:2110659

A;Accession: S09258

A;Molecule type: DNA

A;Residues: 1-138 <HAM>

A;Cross-references: EMBL:X51719; NID:g53207; PIDN:CAA36012.1; PID:g297545

C;Genetics:

A;Introns: 16/1

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 79.7%; Score 573; DB 2; Length 138;
 Best Local Similarity 80.4%; Pred. No. 1.4e-42;
 Matches 111; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

```

Qy      1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
        |||:||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1 MNFGLSLIFLVLIILKGVQCEVILVESGGGLVKPGGSLKLSCAASGFTFSYTMSWVRQTP 60

Qy      61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
        :|||:| ||| || |:|||||:|||| |||||:||||| ||
Db      61 EKRLEWVATISSGGGNTYYPDSVKGRFTISRDNAKNNLYLQMSSLRSEDTALYYCARYYR 120

Qy      121 YSGSSDYWGQGTTVTVSS 138
        | |||| |||:
Db      121 YEAWFASWGQGTILVTVSA 138
  
```

RESULT 2

B26471

Ig heavy chain precursor V region (MAK33) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 23-Jul-1999

C;Accession: B26471; S70410

R;Buckel, P.; Hubner-Parajsz, C.; Mattes, R.; Lenz, H.; Haug, H.; Beaucamp, K.
 Gene 51, 13-19, 1987

A;Title: Cloning and nucleotide sequence of heavy- and light-chain cDNAs from a
 creatine-kinase-specific monoclonal antibody.

A;Reference number: A91572; MUID:87248058; PMID:3110009

A;Accession: B26471

A;Molecule type: mRNA

A;Residues: 1-152 <BUC>

A;Cross-references: GB:M16163; NID:g195405; PIDN:AAA38292.1; PID:g195406

R;Lebecque, S.G.; Gearhart, P.J.

J. Exp. Med. 172, 1717-1727, 1990

A;Title: Boundaries of somatic mutation in rearranged immunoglobulin genes: 5'
 boundary is near the promoter, and 3' boundary is about 1 kb from V(D)J gene.

A;Reference number: S70410; MUID:91079775; PMID:2258702

A;Accession: S70410

A;Status: translation not shown

A;Molecule type: DNA

A;Residues: 1-19 <LEB>

A;Cross-references: EMBL:X53776; NID:g52475; PIDN:CAA37792.1; PID:g52476

C;Genetics:

A;Introns: 16/1

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;1-19/Domain: signal sequence #status predicted <SIG>

F;20-152/Product: Ig heavy chain V region MAK33 #status predicted <MAT>

F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 79.1%; Score 569; DB 2; Length 152;
 Best Local Similarity 78.2%; Pred. No. 3.5e-42;
 Matches 111; Conservative 10; Mismatches 17; Indels 4; Gaps 1;

```

Qy      1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
        |||:||||| ||||| ||||| ||||| ||||| ||||| |||||
  
```

```

Db          1 MNFGLSLIFLVLVLKGVQCEVQGVESGGGLVKPGGSLKLSCAASGFTFSDYYMYWVRQTP 60
Qy          61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVR--- 117
              :|||||:|  ||  ||| |:|||||||:|||| | |||||:|||| |
Db          61 EKRLEWVATISDGGSYTYYPDSVKGRFTISRDNAKNNLYLQMSSLKSEDTAMYYCARDKA 120
Qy          118 -YDHYSGSSDYWGQGTTVTVSS 138
              | :|  : |||||:||||
Db          121 YYGNYGDAMDYWGQTSVTVSS 142

```

RESULT 3

S38808

Ig heavy chain - mouse

C;Species: Mus musculus (house mouse)

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Jan-2000

C;Accession: S38808

R;Sequeira, A.; Avrameas, S.; Jouvin-Marche, E.

Immunogenetics 36, 15-21, 1992

A;Title: Molecular characterization of the variable regions of a mouse polyreactive IgG2b antibody with rheumatoid factor activity.

A;Reference number: S38807; MUID:92267566; PMID:1587549

A;Accession: S38808

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-139 <SEQ>

A;Cross-references: EMBL:X53400

A;Note: the authors translated the codon GAG for residue 117 as Lys

A;Note: the sequence of residues 134-139 and the corresponding nucleotide sequence are not shown in this paper

C;Superfamily: immunoglobulin V region; immunoglobulin homology

F;34-116/Domain: immunoglobulin homology <IMM>

```

Query Match          77.8%;  Score 559.5;  DB 2;  Length 139;
Best Local Similarity 79.3%;  Pred. No. 2.1e-41;
Matches 111;  Conservative 8;  Mismatches 16;  Indels 5;  Gaps 2;

```

```

Qy          1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
              ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db          1 MNFGFSLIFLVLVLKGVQCEVKLVESGGGLVKPGGSLKLSCAASGFTFSSYAMSWVRQTP 60
Qy          61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
              :||||||| | ||  ||| |:|||||||:|:| | |||||:||||:| | |
Db          61 EKRLEWVASI-SRGGTTYYPDSVKGRFTISRDNARNNLYLQMSSLRSEDAMYYCAREGI 119
Qy          121 YSG----SSDYWGQGTTVTV 136
              | |  |||||:| |
Db          120 YGYALYGM DYWGQTSVTV 139

```

RESULT 4

C34903

Ig heavy chain precursor V region (5-27) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 16-Aug-1996

C;Accession: C34903

R;Bedzyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.

F;34-119/Domain: immunoglobulin homology <IMM>

F;34-117/Domain: immunoglobulin homology <IMM>

Qy 61 DKRLEWVASIRSGGGRTYYSNDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120

Db 61 GKGLEWVAFIRYDGSNKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAR-DH 119

Qy 121 YSGSS--DYWGQGT TVTVSS 138
|:: ||||| |||||

Db 120 IVGATYFDYWGQGT LVTVSS 139

RESULT 6

S31686

Ig heavy chain V region - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C;Accession: S31686

R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992

A;Description: Mechanisms that generate human immunoglobulin diversity operate
from the 8th week of gestation in feral liver.

A;Reference number: S31585

A;Accession: S31686

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-140 <CUI>

A;Cross-references: EMBL:Z14205; NID:g30969; PIDN:CAA78574.1; PID:g30970

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 71.9%; Score 517; DB 2; Length 140;
Best Local Similarity 70.7%; Pred. No. 9.9e-38;
Matches 99; Conservative 17; Mismatches 22; Indels 2; Gaps 1;

Qy 1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
| |||| : || :|||||||:|:|||||||:| ||:|||||||:| |||||

Db 1 MEFGLSWLSLVAILKGVQCEVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAP 60

Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISR ENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
| ||||:| || |||||:|||||||:|:|||||||:|:|||||:| :

Db 61 GKGLEWVSAISGSGGSTYYSDSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKCPF 120

Qy 121 YSGSS--DYWGQGT TVTVSS 138
|| ||||| |||||

Db 121 AGGSPSFDYWGQGT LVTVSS 140

RESULT 7

S05271

Ig heavy chain precursor - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 16-Aug-1996

C;Accession: S05271; S04602

R;Kishimoto, T.

submitted to the EMBL Data Library, March 1989

A;Reference number: S05270

A;Accession: S05271

A;Molecule type: mRNA

A;Residues: 1-160 <KIS1>

A;Cross-references: EMBL:X14584

R;Kishimoto, T.; Okajima, H.; Okumoto, T.; Taniguchi, M.

Nucleic Acids Res. 17, 4385, 1989

A;Title: Nucleotide sequences of the cDNAs encoding the V-regions of H- and L-chains of a human monoclonal antibody with broad reactivity to malignant tumor cells.

A;Reference number: S04601; MUID:89296497; PMID:2500644

A;Accession: S04602

A;Molecule type: mRNA

A;Residues: 1-144 <KIS2>

A;Cross-references: EMBL:X14584

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;1-19/Domain: signal sequence #status predicted <SIG>

F;20-160/Product: Ig heavy chain (fragment) #status predicted <MAT>

F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 71.8%; Score 516; DB 2; Length 160;

Best Local Similarity 68.1%; Pred. No. 1.4e-37;

Matches 98; Conservative 18; Mismatches 22; Indels 6; Gaps 1;

Qy 1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
| |||| :|| :|||||||:|:|||||||:| ||:||||||| | |||||

Db 1 MEFGLSWLFLVAILKGVQCEVQLLESGGGLVQPGGSLRLSCAASGFTFSTYAMSWVRQAP 60

Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVR--- 117
| ||||::| || |||:|:|||||||:|:|||||||:|:|:||||:| | :

Db 61 GKGLEWVSAISGSGGSTYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKAVV 120

Qy 118 ---YDHYSGSSDYWGQGTTVTVSS 138

:| | |||||||||

Db 121 RGVISYYYYGMDVWGQGTTVTVSS 144

RESULT 8

S31699

Ig heavy chain V region - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C;Accession: S31699

R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelles, C.
submitted to the EMBL Data Library, June 1992

A;Description: Mechanisms that generate human immunoglobulin diversity operate from the 8th week of gestation in feral liver.

A;Reference number: S31585

A;Accession: S31699

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-134 <CUI>

A;Cross-references: EMBL:Z14201; NID:g30961; PIDN:CAA78570.1; PID:g30962

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 71.5%; Score 514; DB 2; Length 134;

Best Local Similarity 71.0%; Pred. No. 1.7e-37;

Matches 98; Conservative 16; Mismatches 20; Indels 4; Gaps 1;

```

Qy      1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
      | | | | : | | : | | | | | | : | | | | | | | | | | | | | | | |
Db      1 MEFGLSWLFLVAILKGVQCEVQLLESGGGLVHPGGSRLRLSCAASGFTFSYAMSWVRQAP 60

Qy      61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
      | | | | : | | | | | | | | | | | | | | | | | | | | | | | |
Db      61 GKGLEWVSAISGSGGSTYYSDSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARW-- 118

Qy      121 YSGSSDYWGQGT TVTVSS 138
      | | | | | | | | | |
Db      119 --RDL DYWGQGT LVTVSS 134

```

RESULT 9

S31588

Ig heavy chain V region - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C;Accession: S31588

R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992

A;Description: Mechanisms that generate human immunoglobulin diversity operate
from the 8th week of gestation in feral liver.

A;Reference number: S31585

A;Accession: S31588

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-140 <CUI>

A;Cross-references: EMBL:Z14200; NID:g30957; PIDN:CAA78569.1; PID:g30958

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;34-117/Domain: immunoglobulin homology <IMM>

```

Query Match          71.3%; Score 513; DB 2; Length 140;
Best Local Similarity 69.3%; Pred. No. 2.2e-37;
Matches 97; Conservative 20; Mismatches 21; Indels 2; Gaps 1;

```

```

Qy      1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
      | | | | : | | : | | | | | | : | | | | | | | | | | | | | | | |
Db      1 MEFGLSWLFLVAILRGVQCEVQLLESGGGLVQPGGSRLRLSCAASGFTFSYAMSWVRQAP 60

Qy      61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
      | | | | : | | | | | | | | | | | | | | | | | | | | | | | |
Db      61 GKGLEWVSAISGSGGSTYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCAKDHD 120

Qy      121 YSG--SSDYWGQGT TVTVSS 138
      | | | | | | | | | |
Db      121 YSNYIYFDYWGQGT LVTVSS 140

```

RESULT 10

HVMS84

Ig heavy chain precursor V region (5-84) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 31-Mar-1997

C;Accession: JT0505

R;Levy, N.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart, P.J.

J. Exp. Med. 169, 2007-2019, 1989

A;Title: Early onset of somatic mutation in immunoglobulin VH genes during the primary immune response.

A;Reference number: JT0501; MUID:89279149; PMID:2499654

A;Accession: JT0505

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-117 <LEV>

A;Experimental source: strain BALB/cJ

A;Note: this sequence belongs to the VH7183 subfamily

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;1-19/Domain: signal sequence #status predicted <SIG>

F;20-117/Product: Ig heavy chain V region (5-84) #status predicted <MAT>

F;34-117/Domain: immunoglobulin homology <IMM>

F;41-115/Disulfide bonds: #status predicted

Query Match 71.2%; Score 512; DB 1; Length 117;

Best Local Similarity 84.6%; Pred. No. 2.2e-37;

Matches 99; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

Qy 1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60

||||| :||| ||||| :||| ||||| :||| ||||| :||| |||||

Db 1 MNFGLSLIFLVLVLKGVLCCEVKLVESGGGLVQPGGSLKLSCAASGFTFSYTMWVRQTP 60

Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVR 117

:||| ||| :||| ||| ||||| :||| ||||| :||| |||

Db 61 EKRLEWVAYISNGGGSTYYPDTVKGRFTISRDNAKNNLYLQMSSLKSEDTAMYCAR 117

RESULT 11

HVMS34

Ig heavy chain precursor V region (345) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 31-Mar-1997

C;Accession: JT0502

R;Levy, N.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart, P.J.

J. Exp. Med. 169, 2007-2019, 1989

A;Title: Early onset of somatic mutation in immunoglobulin VH genes during the primary immune response.

A;Reference number: JT0501; MUID:89279149; PMID:2499654

A;Accession: JT0502

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-117 <LEV>

A;Experimental source: strain BALB/cJ

A;Note: this sequence belongs to the VH7183 subfamily

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;1-19/Domain: signal sequence #status predicted <SIG>

F;20-117/Product: Ig heavy chain V region (345) #status predicted <MAT>

F;34-117/Domain: immunoglobulin homology <IMM>

F;41-115/Disulfide bonds: #status predicted

Query Match 70.9%; Score 510; DB 1; Length 117;

Best Local Similarity 83.8%; Pred. No. 3.3e-37;

Matches 98; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

```

Qy      1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
        ||||| ||||| ||||:||||:||||||| ||||| ||:| |||||
Db      1 MNFGLRLIFLVLTLKGVKCEVQLVESGGGLVKPGGSLKLSCAASGFAFSSYDMSWVRQTP 60

Qy      61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVR 117
        :||||||| | ||| ||| | |||||:||||||| |||||:||| |
Db      61 EKRLEWVAYISSGGGSTYYPDTVKGRFTISRDNKNTLYLQMSSLKSEDTAMYVCAR 117

```

RESULT 12

S31615

hypothetical protein - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999

C;Accession: S31615

R;Recinos, A.; Silvey, K.J.; Jensen, R.H.; Stanker, L.H.

submitted to the EMBL Data Library, April 1991

A;Description: Immunoglobulin variable heavy and light chain cDNA sequences for antidioxin monoclonal.

A;Reference number: S31615

A;Accession: S31615

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-136 <REC>

A;Cross-references: EMBL:X58884; NID:g51824; PIDN:CAA41688.1; PID:g51825

C;Superfamily: immunoglobulin V region; immunoglobulin homology

F;34-117/Domain: immunoglobulin homology <IMM>

```

Query Match          70.7%; Score 508; DB 2; Length 136;
Best Local Similarity 70.3%; Pred. No. 5.8e-37;
Matches 97; Conservative 16; Mismatches 23; Indels 2; Gaps 1;

```

```

Qy      1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
        ||||| ||||| |||||:| ||||| |||||:||||:|||| || | ||||
Db      1 MNFGLRLIFLVLTLKGVQCDVNLVESGGGLVKPGGTLKLSCSASGFAFSTYSMVWVRQTP 60

Qy      61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
        :|||||||:| || ||| |:|:|||||||:|:| || | |:| |||||:|||| |
Db      61 EKRLEWVATITGGGTYTYPPDSVRGRFTISRDNARDTLNLHMTNLKSEDTAMYCYCLGYW 120

Qy      121 YSGSSDYWGQGTTVTVSS 138
        | |: ||||| |||:
Db      121 YDGT--YWGQGLVIVSA 136

```

RESULT 13

S22657

Ig heavy chain precursor V region (0-81VH) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 06-Feb-1998

C;Accession: S22657

R;Hirabayashi, Y.; Munakata, Y.; Sasaki, T.; Sano, H.

Nucleic Acids Res. 20, 2601, 1992

A;Title: Variable regions of a human anti-DNA antibody O-81 possessing lupus nephritis-associated idiotype.

A;Reference number: S22657; MUID:92285150; PMID:1598223

A;Accession: S22657
 A;Molecule type: mRNA
 A;Residues: 1-140 <HIR>
 A;Cross-references: EMBL:X59134
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;1-19/Domain: signal sequence #status predicted <SIG>
 F;20-140/Product: Ig heavy chain (fragment) #status predicted <MAT>
 F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 70.1%; Score 504; DB 2; Length 140;
 Best Local Similarity 68.1%; Pred. No. 1.3e-36;
 Matches 94; Conservative 21; Mismatches 19; Indels 4; Gaps 1;

```

Qy      1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
      | ||| :|| :|:|||||:|||||||:| ||:|||||||:|: |||
Db      1 MEFGLSWFLVAILEGVQCEVQLVESGGGLVQPGGSLRLSCAASGFTFSSHWMTWVRQTP 60

Qy     61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSLKS EDTALYYCVRYDH 120
      |||||:|: | ||:|:|:|||||:||||:|||| | |:|:|:| |
Db     61 GKRLEWVANVKQDGSARYYADSVRGRFTISRDNAKNSLYLQMDSLRADDTAVYYCAR--- 117

Qy    121 YSGSSDYWGQGT TVTVSS 138
      | ||||| ||||
Db    118 -STGIDYWGQGT LVTVSS 134
  
```

RESULT 14

G1MS21

Ig heavy chain precursor V region (MOPC 21) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 22-Jun-1999

C;Accession: E90809; A93184; A02066

R;Bothwell, A.L.M.; Paskind, M.; Reth, M.; Imanishi-Kari, T.; Rajewsky, K.; Baltimore, D.

Cell 24, 625-637, 1981

A;Title: Heavy chain variable region contribution to the NP(b) family of antibodies: somatic mutation evident in a gamma2a variable region.

A;Reference number: A90809; MUID:81234548; PMID:6788376

A;Accession: E90809

A;Molecule type: mRNA

A;Residues: 1-136 <BOT>

A;Cross-references: GB:J00522; NID:g195052; PIDN:AAD15290.1; PID:g195055

R;Adetugbo, K.; Milstein, C.; Secher, D.S.

Nature 265, 299-304, 1977

A;Title: Molecular analysis of spontaneous somatic mutants.

A;Reference number: A93184; MUID:77100368; PMID:401950

A;Contents: myeloma protein MOPC 21

A;Accession: A93184

A;Molecule type: protein

A;Residues: 17-74,'D',76-77,'H',79-88,'ND',91-114,'H',116-119,'W',121-136 <ADE>

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;1-16/Domain: signal sequence (fragment) #status predicted <SIG>

F;17-136/Product: Ig heavy chain V region (MOPC 21) #status experimental <MAT>

F;31-114/Domain: immunoglobulin homology <IMM>

F;115-119/Region: D segment

F;120-136/Region: J segment (JH4)
F;38-112/Disulfide bonds: #status experimental

Query Match 69.9%; Score 502.5; DB 1; Length 136;
Best Local Similarity 70.4%; Pred. No. 1.7e-36;
Matches 95; Conservative 20; Mismatches 19; Indels 1; Gaps 1;

Qy 5 LSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNSDKRL 64
|:|:||||:|||||:|:|||||||:| | |||||:|:| | ||| :| |
Db 2 LNLVFLVLILKGVQCDVLVESGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGL 61

Qy 65 EWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSLKSSEDALYYCVRYDHYS-G 123
||| | || :|:| |||||:| |||:|:|:|:|:|:| | :|
Db 62 EWWAYISSGSSTLHYADTVKGRFTISRDNPKNTLFLQMTSLRSEDAMYYCARWGNYPY 121

Qy 124 SSDYWGQGT TVTVSS 138
: |||||:|||||
Db 122 AMDYWGQGT SVTVSS 136

RESULT 15

S31666

Ig heavy chain V region - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C;Accession: S31666

R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelles, C.
submitted to the EMBL Data Library, June 1992

A;Description: Mechanisms that generate human immunoglobulin diversity operate
from the 8th week of gestation in feral liver.

A;Reference number: S31585

A;Accession: S31666

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-138 <CUI>

A;Cross-references: EMBL:Z14202; NID:g30963; PIDN:CAA78571.1; PID:g30964

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 69.8%; Score 502; DB 2; Length 138;
Best Local Similarity 67.6%; Pred. No. 1.9e-36;
Matches 96; Conservative 21; Mismatches 17; Indels 8; Gaps 2;

Qy 1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
| |||| :||| :|||||||:|:|||||||:| | ||:|||||||:| | |||||
Db 1 MEFGLSWLFLVAILKGVQCEVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAP 60

Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSLKSSEDALYYCVR--- 117
| ||||:| | |||:|:|||||||:|:|||||||:|:|:|:|:| :
Db 61 GKGLEWVSAISGGGSTYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKART 120

Qy 118 -YDHYSGSSDYWGQGT TVTVSS 138
| :: | ||:| |||||
Db 121 GYWF----DLWGRGTLVTVSS 138

Search completed: May 17, 2004, 11:33:09
Job time : 14.8 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 17, 2004, 11:32:34 ; Search time 39.3556 Seconds
(without alignments)
975.722 Million cell updates/sec

Title: US-10-010-942B-4
Perfect score: 719
Sequence: 1 MNFGLSLIFLVVLKGVQCE.....DHYSGSSDYWGQTTVTVSS 138

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1145568 seqs, 278261457 residues

Total number of hits satisfying chosen parameters: 1145568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					
No.	Score	Match	Length	DB	ID	Description

1	719	100.0	138	14	US-10-010-942B-4	Sequence 4, Appli
2	719	100.0	138	16	US-10-388-389-4	Sequence 4, Appli
3	652	90.7	138	14	US-10-010-942B-8	Sequence 8, Appli
4	652	90.7	138	16	US-10-388-389-8	Sequence 8, Appli
5	650	90.4	138	14	US-10-010-942B-12	Sequence 12, Appl
6	650	90.4	138	16	US-10-388-389-12	Sequence 12, Appl
7	609.5	84.8	133	13	US-10-006-773-9	Sequence 9, Appli
8	578.5	80.5	139	13	US-10-006-773-17	Sequence 17, Appl
9	578	80.4	462	14	US-10-281-479A-23	Sequence 23, Appl
10	578	80.4	462	14	US-10-286-132A-23	Sequence 23, Appl
11	578	80.4	464	14	US-10-275-180A-23	Sequence 23, Appl
12	569	79.1	144	9	US-09-881-823-12	Sequence 12, Appl
13	566	78.7	140	9	US-09-286-240-4	Sequence 4, Appli
14	559	77.7	140	13	US-10-006-773-4	Sequence 4, Appli
15	557.5	77.5	137	9	US-09-423-800-76	Sequence 76, Appl
16	557.5	77.5	137	14	US-10-337-981-76	Sequence 76, Appl
17	553	76.9	158	12	US-10-226-795-32	Sequence 32, Appl
18	549	76.4	140	14	US-10-283-349-23	Sequence 23, Appl
19	542	75.4	140	12	US-10-365-123-51	Sequence 51, Appl
20	537	74.7	159	15	US-10-291-265-333	Sequence 333, App
21	531.5	73.9	143	11	US-09-791-551-117	Sequence 117, App
22	522	72.6	313	15	US-10-291-265-427	Sequence 427, App
23	522	72.6	470	16	US-10-038-591-46	Sequence 46, Appl
24	520.5	72.4	469	12	US-10-292-088-54	Sequence 54, Appl
25	514.5	71.6	139	10	US-09-947-839-96	Sequence 96, Appl
26	514	71.5	138	9	US-09-796-744-15	Sequence 15, Appl
27	514	71.5	138	14	US-10-231-452-62	Sequence 62, Appl
28	512	71.2	465	14	US-10-401-344-2	Sequence 2, Appli
29	510.5	71.0	137	9	US-09-423-800-77	Sequence 77, Appl
30	510.5	71.0	137	14	US-10-337-981-77	Sequence 77, Appl
31	510.5	71.0	473	16	US-10-038-591-50	Sequence 50, Appl
32	508.5	70.7	307	15	US-10-291-265-332	Sequence 332, App
33	508.5	70.7	363	15	US-10-291-265-335	Sequence 335, App
34	506	70.4	474	10	US-09-848-832-3	Sequence 3, Appli
35	506	70.4	474	14	US-10-225-108A-3	Sequence 3, Appli
36	506	70.4	474	15	US-10-461-148-1	Sequence 1, Appli
37	503.5	70.0	471	12	US-10-292-088-6	Sequence 6, Appli
38	503	70.0	312	15	US-10-291-265-334	Sequence 334, App
39	503	70.0	470	12	US-10-292-088-62	Sequence 62, Appl
40	500.5	69.6	137	15	US-10-443-466A-45	Sequence 45, Appl
41	500	69.5	470	16	US-10-038-591-45	Sequence 45, Appl
42	500	69.5	470	16	US-10-038-591-49	Sequence 49, Appl
43	499	69.4	367	15	US-10-291-265-899	Sequence 899, App
44	498.5	69.3	467	12	US-10-180-648-2	Sequence 2, Appli
45	498	69.3	140	15	US-10-443-466A-27	Sequence 27, Appl

ALIGNMENTS

RESULT 1

US-10-010-942B-4

; Sequence 4, Application US/10010942B

; Publication No. US20030165496A1

; GENERAL INFORMATION:

; APPLICANT: Basi, Guriq

```
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002
; CURRENT APPLICATION NUMBER: US/10/010,942B
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(19)
US-10-010-942B-4
```

```
Query Match          100.0%; Score 719; DB 14; Length 138;
Best Local Similarity 100.0%; Pred. No. 8.5e-61;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
        |||
Db      1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60

Qy      61 DKRLEWVASIRSGGGRITYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
        |||
Db      61 DKRLEWVASIRSGGGRITYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120

Qy      121 YSGSSDYWGQGTTTVTVSS 138
        |||
Db      121 YSGSSDYWGQGTTTVTVSS 138
```

RESULT 2

```
US-10-388-389-4
; Sequence 4, Application US/10388389
; Publication No. US2004008777A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Guriq
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA-AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002CP
; CURRENT APPLICATION NUMBER: US/10/388,389
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
```



```

Qy      1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
        |||:|||||:| ||:|||||
Db      1 MNFGLSLIFLVVLKGVQCEVQLLES GGGLVQPGGSLRLSCAASGFTFSNYGMSWVRQAP 60

Qy      61 DKRLEWVASIRSGGGRYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
        | |||:|||||:|||||:|||||:| ||:|||||
Db      61 GKGLEWVASIRSGGGRYYSDNVKGRFTISRDNKNSLYLQMNSLRAEDTALYYCVRYDH 120

Qy      121 YSGSSDYWGQGT TVTVSS 138
        |||:|||||
Db      121 YSGSSDYWGQGT LVTVSS 138

```

RESULT 4

```

US-10-388-389-8
; Sequence 8, Application US/10388389
; Publication No. US20040087777A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Guriq
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA-AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002CP
; CURRENT APPLICATION NUMBER: US/10/388,389
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized 3D6 heavy chain variable region
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(19)
US-10-388-389-8

```

```

Query Match          90.7%; Score 652; DB 16; Length 138;
Best Local Similarity 89.1%; Pred. No. 2.1e-54;
Matches 123; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

```

```

Qy      1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
        |||:|||||:| ||:|||||
Db      1 MNFGLSLIFLVVLKGVQCEVQLLES GGGLVQPGGSLRLSCAASGFTFSNYGMSWVRQAP 60

Qy      61 DKRLEWVASIRSGGGRYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
        | |||:|||||:|||||:|||||:| ||:|||||
Db      61 GKGLEWVASIRSGGGRYYSDNVKGRFTISRDNKNSLYLQMNSLRAEDTALYYCVRYDH 120

Qy      121 YSGSSDYWGQGT TVTVSS 138
        |||:|||||

```



```
; TITLE OF INVENTION: BETA-AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002CP
; CURRENT APPLICATION NUMBER: US/10/388,389
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized 3D6 light chain variable region
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(19)
US-10-388-389-12
```

```
Query Match          90.4%; Score 650; DB 16; Length 138;
Best Local Similarity 88.4%; Pred. No. 3.2e-54;
Matches 122; Conservative 10; Mismatches 6; Indels 0; Gaps 0;
```

```
Qy      1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
      |||
Db      1 MNFGLSLIFLVVLKGVQCEVQLLES GGGLVQPGGSLRLSCAASGFTFSNYGMSWVRQAP 60
      |||

Qy      61 DKRLEWVASIRSGGRTYYSDNVKGRFTISR ENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
      | |||
Db      61 GKGLEWVASIRSGGRTYYSDNVKGRFTISR DNSKNTLYLQMNSLRAEDTAVYYCVRYDH 120
      |||

Qy      121 YSGSSDYWGQGT TVTVSS 138
      |||
Db      121 YSGSSDYWGQGT LTVTVSS 138
      |||
```

RESULT 7

US-10-006-773-9

```
; Sequence 9, Application US/10006773
; Publication No. US20020132983A1
; GENERAL INFORMATION:
; APPLICANT: Junghans, Richard P.
; TITLE OF INVENTION: Antibodies as Chimeric Effector Cell Receptors Against
Tumor Antigens
; FILE REFERENCE: 003
; CURRENT APPLICATION NUMBER: US/10/006,773
; CURRENT FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: 60/250,089
; PRIOR FILING DATE: 2000-11-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Mus. sp.
```

US-10-006-773-9

Query Match 84.8%; Score 609.5; DB 13; Length 133;
Best Local Similarity 87.0%; Pred. No. 2.2e-50;
Matches 120; Conservative 6; Mismatches 7; Indels 5; Gaps 1;

```
Qy      1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
        |||||||||||||||||||:|||||||||||||||||||||
Db      1 MNFGLSLIFLVVLKGVQCEVKVVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQTS 60

Qy     61 DKRLEWVASIRSGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
        ||||||||| ||| |:|||||||||||||||||||||||||||
Db     61 DKRLEWVASISSGGDSTFYADNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCARDL 120

Qy     121 YSGSSDYWGQGTTVTVSS 138
        :: |||||:||||
Db     121 FN-----WGQGTTLTVSS 133
```

RESULT 8

US-10-006-773-17

; Sequence 17, Application US/10006773

; Publication No. US20020132983A1

; GENERAL INFORMATION:

; APPLICANT: Junghans, Richard P.

; TITLE OF INVENTION: Antibodies as Chimeric Effector Cell Receptors Against Tumor Antigens

; FILE REFERENCE: 003

; CURRENT APPLICATION NUMBER: US/10/006,773

; CURRENT FILING DATE: 2001-12-10

; PRIOR APPLICATION NUMBER: 60/250,089

; PRIOR FILING DATE: 2000-11-30

; NUMBER OF SEQ ID NOS: 19

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 17

; LENGTH: 139

; TYPE: PRT

; ORGANISM: Mus sp.

US-10-006-773-17

Query Match 80.5%; Score 578.5; DB 13; Length 139;
Best Local Similarity 82.7%; Pred. No. 2.1e-47;
Matches 115; Conservative 6; Mismatches 17; Indels 1; Gaps 1;

```
Qy      1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
        |||||||||||||||||||:|||||||||||||||||||||
Db      1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLMNPASLKLSCAASGFSFSNYGMSWVRQTS 60

Qy     61 DKRLEWVASIRSGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
        ||||||||| :|| |:|||||||||||||||||||||||||||
Db     61 DKRLEWVASISTGGANTFYDPNVKGRFTISRENAKNTLYLQMSSLKSEDTALYFCARDSH 120

Qy     121 YSGS-SDYWQGTTVTVSS 138
        | ||||| |||:
Db     121 SVGCWFATWGQGTTLTVSA 139
```

US-10-281-479A-23

Query Match 80.4%; Score 578; DB 14; Length 462;
Best Local Similarity 81.2%; Pred. No. 8.9e-47;
Matches 112; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

RESULT 10


```
; APPLICANT: Koopman, William J.
; TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED
APOPTOSIS-
; TITLE OF INVENTION: INDUCING LIGAND RECEPTOR AND USES THEREOF
; FILE REFERENCE: 21085.0029U5
; CURRENT APPLICATION NUMBER: US/10/275,180A
; CURRENT FILING DATE: 2002-10-31
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 23
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/No. US20030190687A1e
=
; OTHER INFORMATION: Synthetic Construct
US-10-275-180A-23
```

```
Query Match          80.4%; Score 578; DB 14; Length 464;
Best Local Similarity 81.2%; Pred. No. 9e-47;
Matches 112; Conservative 10; Mismatches 16; Indels 0; Gaps 0;
```

```
Qy      1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
      |||
Db      1 MNFGLSLIFLVVLKGVQCEVMLVESGGGLVKPGGSLKLSCAASGFTFSSYVMSWVRQTP 60

Qy      61 DKRLEWVASIRSGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
      :|||
Db      61 EKRLEWVATISSGGSYTYYPDSVKGRFTISRDNKNTLYLQMSSLRSEDTAMYYCARRGD 120

Qy      121 YSGSSDYWGQGTTTVTVSS 138
      ::|||
Db      121 SMITTDYWGQGTTLTVSS 138
```

RESULT 12

```
US-09-381-823-12
; Sequence 12, Application US/09881823
; Patent No. US20020068066A1
; GENERAL INFORMATION:
; APPLICANT: SHI, WENYUAN
; APPLICANT: ANDERSON, MAXWELL
; APPLICANT: MORRISON, SHERIE
; APPLICANT: TRINH, RYAN
; APPLICANT: WIMS, LETITIA
; APPLICANT: CHEN, LI
; TITLE OF INVENTION: Method for the Treatment and Prevention of Dental Caries
; FILE REFERENCE: 22851-032
; CURRENT APPLICATION NUMBER: US/09/881,823
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 07/378,577
; PRIOR FILING DATE: 1999-08-20
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 144
```

; TYPE: PRT
; ORGANISM: Murine
US-09-881-823-12

Query Match 79.1%; Score 569; DB 9; Length 144;
Best Local Similarity 78.2%; Pred. No. 1.7e-46;
Matches 111; Conservative 11; Mismatches 16; Indels 4; Gaps 1;

```
Qy      1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
          |:|||||:|||| ||||||:||||||| || ||||||:| |||||
Db      1 MDFGLSLVFLVLTLLKGVQCDVKLVESGGGLVNPGGSLKLSCAASGFTFSSYTMSWVRQTP 60

Qy     61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVR--- 117
          :||||||| ||| ||| |:|||||||:|||||||:|||||||:| |||
Db     61 EKRLEWVASISSGGTYTYYPDSVKGRFTISRDNAKNTLYLQMTSLKSEDTAMYYCSRDDG 120

Qy    118 -YDHYSGSSDYWGQGT TVTVSS 138
          | | : |||||:|||||
Db    121 SYGSYYYAMDYWGQGT SVTVSS 142
```

RESULT 13

US-09-286-240-4
; Sequence 4, Application US/09286240
; Patent No. US20020010320A1
; GENERAL INFORMATION:
; APPLICANT: Fett, James W
; TITLE OF INVENTION: Chimeric and Humanized Antibodies to Angiogenin
; FILE REFERENCE: 10498/74073
; CURRENT APPLICATION NUMBER: US/09/286,240
; CURRENT FILING DATE: 1999-04-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-286-240-4

Query Match 78.7%; Score 566; DB 9; Length 140;
Best Local Similarity 79.3%; Pred. No. 3.2e-46;
Matches 111; Conservative 13; Mismatches 14; Indels 2; Gaps 2;

```
Qy      1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
          |:|||| :|||:|||||| |||||||| ||||||||:| |||||
Db      1 MDFGLSWVFLVLILKGVQCEVMLVESGGGLVKPGGSLKLSCAASGFTFSSYTMSWVRQTP 60

Qy     61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRY-D 119
          :||||||:| ||| ||| |:|||||||: ||||||||:||||||| | |
Db     61 EKRLEWVATISSGGGNYYYPDSVKGRFTISRDIKNTLYLQMSSLRSEDTALYYCTRLGD 120

Qy    120 H-YSGSSDYWGQGT TVTVSS 138
          : |: : |||||:|||||
Db    121 YGYAYTMDYWGQGT SVTVSS 140
```

RESULT 14

US-10-006-773-4

; Sequence 4, Application US/10006773
; Publication No. US20020132983A1
; GENERAL INFORMATION:
; APPLICANT: Junghans, Richard P.
; TITLE OF INVENTION: Antibodies as Chimeric Effector Cell Receptors Against
Tumor Antigens
; FILE REFERENCE: 003
; CURRENT APPLICATION NUMBER: US/10/006,773
; CURRENT FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: 60/250,089
; PRIOR FILING DATE: 2000-11-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-006-773-4

Query Match 77.7%; Score 559; DB 13; Length 140;
Best Local Similarity 77.9%; Pred. No. 1.5e-45;
Matches 109; Conservative 9; Mismatches 20; Indels 2; Gaps 1;

Qy 1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
| | | | | : | | | | | | | | | | | | | | | | | | | | | |
Db 1 MNFGFSLIFLVVLKGVQCEVVVVESGGGFVKPGGSLKLSCAAAGFTFSRYAMSWVRQTP 60

Qy 61 DKRLEWVASIRSGGRTYYSNDVKGRFTISRENAKNTLYLQMSLKSSED TALYYCVR--Y 118
: | | | | | : | | | | | | | | | | | | | | | | | | | | | |
Db 61 EKRLEWVATISSGGSHTYYPDSVKGRFTISRDNAKNTLYLQMSLRSSED TAIYYCARPGY 120

Qy 119 DHYSGSSDYWGQGT TTVTVSS 138
| : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 121 DRGAFFDVGAGT TTVTVSS 140

RESULT 15

US-09-423-800-76

; Sequence 76, Application US/09423800
; Patent No. US20020165363A1
; GENERAL INFORMATION:
; APPLICANT: SATO, KOH
; APPLICANT: TSUNENARI, TOSHIKI
; APPLICANT: ISHII, KIMIE
; TITLE OF INVENTION: CACHEXIA REMEDY
; FILE REFERENCE: 04853-0036
; CURRENT APPLICATION NUMBER: US/09/423,800
; CURRENT FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: PCT/JP98/02116
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: JP 125505/1997
; PRIOR FILING DATE: 1997-05-15
; PRIOR APPLICATION NUMBER: JP 194445/1997
; PRIOR FILING DATE: 1997-07-18
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn Ver. 2.1

```
; SEQ ID NO 76
;   LENGTH: 137
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-423-800-76
```

Query Match 77.5%; Score 557.5; DB 9; Length 137;
Best Local Similarity 78.3%; Pred. No. 2e-45;
Matches 108; Conservative 12; Mismatches 17; Indels 1; Gaps 1;

```
Qy      1 MNFGLSLIFLVLVLKGVQCSEVKLVESGGGLVKPGASLKLSAASGFTFSNYGMSWVRQNS 60
        ||||| | : ||||| : ||||| ||||| ||||| ||||| : ||||| : ||
Db      1 MNFGLSLIFLALILKGVQCSEVQLVESGGDLVKPGGSLKLSCAASGFTFSSYGMSWIRQTP 60

Qy     61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRANAKNTLYLQMSSLKSEDALYYCVRYDH 120
        ||||| | : ||| ||| : ||||| ||||| : ||||| ||||| ||||| : : |||
Db     61 DKRLEWVATISSGGSYTYYPDSVKGRFTISRDNAKNTLYLQMSSLKSEDAMFYCARQTT 120

Qy    121 YSGSSDYWGQGTTVTVSS 138
        : : ||||| ||||| :
Db    121 MTYFA-YWGQGTTLTVSA 137
```

Search completed: May 17, 2004, 11:42:06
Job time : 40.3556 secs

OM protein - protein search, using sw model

Run on: May 17, 2004, 11:23:58 ; Search time 36.2889 Seconds
(without alignments)
1199.858 Million cell updates/sec

Title: US-10-010-942B-4
Perfect score: 719
Sequence: 1 MNFGLSLIFLVLVLKGVQCE.....DHYSGSSDYWGQTTVTVSS 138

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertibrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	
No.	Score	Match Length DB ID Description

1	576.5	80.2	487	11	Q99KA4	Q99ka4 mus musculu
2	557	77.5	479	11	Q91WP5	Q91wp5 mus musculu
3	547	76.1	486	11	Q91Z07	Q91z07 mus musculu
4	516.5	71.8	473	11	Q91Z05	Q91z05 mus musculu
5	505	70.2	480	11	Q91XE1	Q91xe1 mus musculu
6	503	70.0	597	4	Q96BB9	Q96bb9 homo sapien
7	492	68.4	119	11	Q920E7	Q920e7 mus musculu
8	490	68.2	499	4	Q8N5K4	Q8n5k4 homo sapien
9	486.5	67.7	613	4	Q8WUK1	Q8wuk1 homo sapien
10	483.5	67.2	573	4	Q8WU38	Q8wu38 homo sapien
11	471	65.5	493	4	Q8NCL6	Q8ncl6 homo sapien
12	461.5	64.2	494	4	Q96K68	Q96k68 homo sapien
13	449	62.4	470	4	Q7Z5W1	Q7z5w1 homo sapien
14	448	62.3	487	11	Q80ZI7	Q80zi7 mus musculu
15	435.5	60.6	469	11	Q8R3V9	Q8r3v9 mus musculu
16	429	59.7	113	4	Q9UL90	Q9ul90 homo sapien
17	426.5	59.3	479	11	Q7TMK4	Q7tmk4 mus musculu
18	418	58.1	121	4	Q9UL71	Q9ul71 homo sapien
19	417.5	58.1	484	11	Q8VEA0	Q8vea0 mus musculu
20	414.5	57.6	112	4	Q9HCC1	Q9hcc1 homo sapien
21	412.5	57.4	147	4	Q9Y509	Q9y509 homo sapien
22	411.5	57.2	118	4	Q9UL91	Q9ul91 homo sapien
23	409.5	57.0	437	11	Q9R1A4	Q9rla4 mus musculu
24	407	56.6	482	4	Q7Z351	Q7z351 homo sapien
25	405	56.3	116	4	Q9UL93	Q9ul93 homo sapien
26	402	55.9	521	4	Q8N4Y9	Q8n4y9 homo sapien
27	401.5	55.8	298	11	Q9QYF0	Q9qyf0 mus musculu
28	397.5	55.3	122	4	Q9UL84	Q9ul84 homo sapien
29	393.5	54.7	118	4	Q9UL72	Q9ul72 homo sapien
30	385	53.5	131	4	Q9UL88	Q9ul88 homo sapien
31	368	51.2	95	4	Q9ULB6	Q9ulb6 homo sapien
32	364	50.6	473	11	Q9D8L4	Q9d8l4 mus musculu
33	351	48.8	168	11	Q8VDC9	Q8vdc9 mus musculu
34	350.5	48.7	463	11	Q99LC4	Q99lc4 mus musculu
35	349	48.5	468	11	Q99L31	Q99l31 mus musculu
36	348	48.4	470	11	Q7TMK1	Q7tmk1 mus musculu
37	348	48.4	484	11	Q99LA6	Q99la6 mus musculu
38	343.5	47.8	145	11	Q924Q7	Q924q7 mus musculu
39	343.5	47.8	482	11	Q8K172	Q8k172 mus musculu
40	340.5	47.4	124	6	Q9N0W4	Q9n0w4 oryctolagus
41	339.5	47.2	278	11	Q921K1	Q921k1 mus musculu
42	337.5	46.9	124	6	Q9N0W6	Q9n0w6 oryctolagus
43	337	46.9	481	11	Q91WT1	Q91wt1 mus musculu
44	336.5	46.8	124	4	Q9UL92	Q9ul92 homo sapien
45	336	46.7	117	11	Q9QXE9	Q9qxe9 mus musculu

ALIGNMENTS

RESULT 1

Q99KA4

ID	Q99KA4	PRELIMINARY;	PRT;	487 AA.
AC	Q99KA4;			
DT	01-JUN-2001 (TrEMBLrel. 17, Created)			
DT	01-JUN-2001 (TrEMBLrel. 17, Last sequence update)			
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)			

DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 4.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 2.
KW Hypothetical protein.
SQ SEQUENCE 479 AA; 51603 MW; ECB2D0877748584F CRC64;

Query Match 77.5%; Score 557; DB 11; Length 479;
Best Local Similarity 78.3%; Pred. No. 9.8e-46;
Matches 108; Conservative 10; Mismatches 16; Indels 4; Gaps 1;

Qy 1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
| | | | : | | | | | | | | | | | | | | | | | | | | | | :
Db 1 MNFGLTLIFLVLTLKGVQCEVQLVESGGGLVKPGGSLKVSCAASGLTFSNYAMSWVRQSP 60

Qy 61 DKRLEWVASIRSGGGRYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
: | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 61 EKRLEWVAAINSNGGNTYYSDTMKGRFTISRDNASTLYLQMSSLRSEDTAFYYCVR--- 117

Qy 121 YSGSSDYWGQGTTVTVSS 138
| | | | |
Db 118 -GGYFDVWGAGTAVTVSS 134

RESULT 3
Q91Z07

ID Q91Z07 PRELIMINARY; PRT; 486 AA.
AC Q91Z07;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC010324; AAH10324.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 4.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 2.
KW Hypothetical protein.
SQ SEQUENCE 486 AA; 52682 MW; 4FEF835125DA870B CRC64;

Query Match 76.1%; Score 547; DB 11; Length 486;
Best Local Similarity 76.2%; Pred. No. 9.3e-45;
Matches 109; Conservative 12; Mismatches 16; Indels 6; Gaps 3;

RESULT 5

Q91XE1

```

ID      Q91XE1      PRELIMINARY;          PRT;    480 AA.
AC      Q91XE1;
DT      01-DEC-2001 (TrEMBLrel. 19, Created)
DT      01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE      Hypothetical protein (Fragment).
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Colon;
RA      Strausberg R.;
RL      Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR      EMBL; BC010798; AAH10798.1; -.
DR      InterPro; IPR007110; Ig-like.
DR      InterPro; IPR003006; Ig_MHC.
DR      InterPro; IPR003596; Ig_v.
DR      Pfam; PF00047; ig; 4.
DR      SMART; SM00406; IGv; 1.
DR      PROSITE; PS50835; IG_LIKE; 4.
DR      PROSITE; PS00290; IG_MHC; 2.
KW      Hypothetical protein.
FT      NON_TER      1      1
SQ      SEQUENCE      480 AA; 51936 MW; 20B9234EEF2B41ED CRC64;

```

Query Match 70.2%; Score 505; DB 11; Length 480;
Best Local Similarity 72.3%; Pred. No. 1.e-40;
Matches 99; Conservative 16; Mismatches 20; Indels 2; Gaps 1;

```

Qy          2  NFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNSD 61
             |||||:|||| |:||||| ||:||||| ||| ||||| :
Db          1  NFGLSLIFLVLILKGVLCVKLVESGGGLVKPGGSLRLSCAASGFIFSNSYMSWVRQTPE 60

Qy          62  KRLEWVASIRSGGRTYSDNVKGRFTISRANAKNTLYLQMSSLKSEDTALYYCVRYDHY 121
             |||||:| :| |:| |:|||||:|:|:| |:|:| ||||:| ||| | |:
Db          61  KRLEWVATISNSGYATHYPDSMKGRFTISRDNAQNTVLLQMTSLNSEDNAVYYCTRGDYW 120

Qy          122 SGSSDYWGQGTTVTVVSS 138
             | || |||||
Db          121 --YFDVWGAGTTTVTVSS 135

```

RESULT 6

Q96BB9

```

ID   Q96BB9          PRELIMINARY;          PRT;    597 AA.
AC   Q96BB9;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)

```

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=B-cell;
 RA Strausberg R.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC015760; AAH15760.1; -.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; ig; 5.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG_LIKE; 5.
 DR PROSITE; PS00290; IG_MHC; 3.
 KW Hypothetical protein.
 SQ SEQUENCE 597 AA; 65039 MW; 4FCA3AD8ECE263D9 CRC64;

Query Match 70.0%; Score 503; DB 4; Length 597;
 Best Local Similarity 66.7%; Pred. No. 2.3e-40;
 Matches 96; Conservative 22; Mismatches 20; Indels 6; Gaps 2;

Qy 1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
 | |||| :||| :|||||||:|:|||||||:| | |:|||||||:|:| | :|||
 Db 1 MEFGLSWLFLVAILKGVQCEVQLLESGGGLVQPGGSLRLSCAASGFSFSSYAMNWVRQAP 60
 Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
 | ||||:| | |||:|:|||||||:|:~:|||||:|:~:||||:| | :
 Db 61 GKGLEWVSAISGSGGSTYYADSVKGRFTISRDN~SRDTLYLQMNSLRAEDTAVYYCAKDPR 120
 Qy 121 -YSGS-----SDYWGQGT~TVTVSS 138
 || | ||||| |||||
 Db 121 GYSASGNYTREDYWGQGT~LVTVSS 144

RESULT 7
 Q920E7

ID Q920E7 PRELIMINARY; PRT; 119 AA.
 AC Q920E7;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Pterin-mimicking anti-idiotope heavy chain variable region
 DE (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Atkin J.D., Iape A., Jennings I.G., Horaitis O., Cotton R.G.H.;
 RT "Definition of the Idiotope of Pterin-Mimicking Antibodies Expressed

RT in Mammalian Cells.";
 RL Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF307937; AAL09421.1; -.
 DR PIR; C25913; C25913.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; ig; 1.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 FT NON_TER 1 1
 FT NON_TER 119 119
 SQ SEQUENCE 119 AA; 13025 MW; F6E904044381CA7C CRC64;

Query Match 68.4%; Score 492; DB 11; Length 119;
 Best Local Similarity 79.0%; Pred. No. 3.7e-40;
 Matches 94; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

Qy 20 EVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNSDKRLEWVASIRSGGGRTYY 79
 ||:||||| ||||| |||||||||:||||| |||||:| ||| |||
 Db 1 EVQLVESGGDLVKPGGSLKLSCAASGFTFSSYGMSWVRQTPDKRLEWVATISSGGSYTY 60
 Qy 80 SDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDHYSGSSDYWGQGT'TVTVSS 138
 |:|||||||:|||||||:||||| |: | ||||| ||||:
 Db 61 PDSVKGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCARHGDYDVGFAIWGQGT'LTVSA 119

RESULT 8

Q8N5K4

ID Q8N5K4 PRELIMINARY; PRT; 499 AA.
 AC Q8N5K4;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RA Strausberg R.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC032249; AAH32249.1; -.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; ig; 4.
 DR SMART; SM00409; IG; 4.
 DR SMART; SM00407; IGc1; 2.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 499 AA; 53376 MW; 93A5C89582054F32 CRC64;

Query Match 68.2%; Score 490; DB 4; Length 499;
Best Local Similarity 67.1%; Pred. No. 3.3e-39;
Matches 98; Conservative 16; Mismatches 24; Indels 8; Gaps 2;

```
Qy      1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
      | ||| :||| :|||||||:|||||||:|:| | |:||| ||| : | |||
Db      1 MEFGLSWVFLVAILKGVQCEVQLVESGGGVVVRPGSLRLSCATSGFTFDDSGASWVRQAP 60

Qy     61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVR--Y 118
      | |||:| | | | |:|:|||||||:||||:||||:|: | ||||| |
Db     61 GKGLEWVSSINWNGGSTNYADSVKGRFTISRDNAKNSLYLQMNSLRVEDTALYYCARDPT 120

Qy     119 DHYSGSS-----DYWGQGTTVTVSS 138
      : || | | ||:|||||||
Db     121 KYCSGGSCLGYYMDVWGKGTTVTVSS 146
```

RESULT 9

Q8WUK1

ID Q8WUK1 PRELIMINARY; PRT; 613 AA.
AC Q8WUK1;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Tonsil;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC020240; AAH20240.1; -.
DR PIR; PL0120; PL0120.
DR PIR; S15590; S15590.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 5.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 613 AA; 67296 MW; 60C7F5950671E315 CRC64;

Query Match 67.7%; Score 486.5; DB 4; Length 613;
Best Local Similarity 67.9%; Pred. No. 9.4e-39;
Matches 95; Conservative 19; Mismatches 23; Indels 3; Gaps 2;

```
Qy      1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
      | ||| :||| :|||||||:|||||||:|:| | |:||| ||| : | |||
Db      1 MEFGLSWVFLVALLRGVQCQVQLVESGGGVVQPGSLRLSCAASGFTFSSYGMHWVRQAP 60

Qy     61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
```

```

      | |||| |   | ||::|||||:::||:|||||:::||:||||:| : |
Db       61 GKGLEWVAVISYDGSNKYYADSVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAK-DW 119

Qy      121 YSG--SSDYWGQGTTVTVSS 138
      | : | |||| |||| 
Db      120 SEGVETFDIWGQGTMTVTVSS 139

```

Q8WU38

```

ID      Q8WU38      PRELIMINARY;      PRT;      573 AA.
AC      Q8WU38;
DT      01-MAR-2002 (TrEMBLrel. 20, Created)
DT      01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE      Hypothetical protein.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Tonsil;
RA      Strausberg R.;
RL      Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
DR      EMBL; BC021276; AAH21276.1; -.
DR      PIR; S21205; S21205.
DR      InterPro; IPR007110; Ig-like.
DR      InterPro; IPR003006; Ig_MHC.
DR      InterPro; IPR003596; Ig_v.
DR      Pfam; PF00047; ig; 4.
DR      SMART; SM00406; IGv; 1.
DR      PROSITE; PS50835; IG_LIKE; 4.
DR      PROSITE; PS00290; IG_MHC; 2.
KW      Hypothetical protein.
SQ      SEQUENCE      573 AA;      62967 MW;      FD072344033AC530 CRC64;

```

Query Match 67.2%; Score 483.5; DB 4; Length 573;
Best Local Similarity 66.9%; Pred. No. 1.7e-38;
Matches 97; Conservative 15; Mismatches 24; Indels 9; Gaps 2;

Qy	1	MNFGSLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS	60
		: : : : : :	
Db	1	MELGLSWIFLLAILKGVQCEVQLVESGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAP	60
Qy	61	DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH	120
		: : : : : : : : :	
Db	61	GKGLEWVSGISWNSGSGIGYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTALYYCAK--H	118
Qy	121	YSGS-----SDYWGGTTTVTVSS	138
Db	119	GSGSYIGYYYYGMDVWGGTTTVTVSS	143

RESULT 11

Q8NCL6

ID Q8NCL6 PRELIMINARY; PRT; 493 AA.

AC Q8NCL6;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein FLJ90170.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Mammary gland;
 RA Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
 RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
 RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K.,
 RA Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
 RA Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;
 RT "NEDO human cDNA sequencing project.";
 RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AK074651; BAC11114.1; -.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; ig; 4.
 DR SMART; SM00409; IG; 4.
 DR SMART; SM00407; IGc1; 2.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 493 AA; 53224 MW; 12ECD7E094777101 CRC64;

Query Match 65.5%; Score 471; DB 4; Length 493;

Best Local Similarity 65.0%; Pred. No. 2.3e-37;

Matches 91; Conservative 19; Mismatches 28; Indels 2; Gaps 1;

Qy 1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
 | |||| :|| :||:||||:|:|||||||:| || ||:||||||| | :| | ||||:
 Db 1 MQFGLSWVFLVALLRGVQCQVQLVESGGGVVLPGGSLRLSCAASGFRFRDYDMHWVRQSP 60

 Qy 61 DKRLEWVASIRSGGGRITYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
 : ||||| | | :||||:|||| |:||:| |||||:| || :||||:|||| |
 Db 61 GEGLEWVALIWYDGTKITYSDSVKGRLTVSRDNYKNTLYLEMKSLGAEDTAVYYCARDQG 120

 Qy 121 YSGSS--DYWGQGTITVTVSS 138
 |:| |:||||| |||||
 Db 121 YAGYGVFDHWGQGTITVTVSS 140

RESULT 12

Q96K68

ID Q96K68 PRELIMINARY; PRT; 494 AA.

AC Q96K68;

DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein FLJ14473.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Mammary gland;
 RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
 RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
 RA Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
 RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
 RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
 RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
 RA Ninomiya K., Iwayanagi T.;
 RT "NEDO human cDNA sequencing project.";
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK027379; BAB55072.1; -.
 DR PIR; S21205; S21205.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; ig; 4.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 494 AA; 53088 MW; 9A1D7AEB5AEE4C0E CRC64;

Query Match 64.2%; Score 461.5; DB 4; Length 494;
 Best Local Similarity 65.5%; Pred. No. 1.9e-36;
 Matches 93; Conservative 16; Mismatches 28; Indels 5; Gaps 2;

QY 1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
 | || :||| |:|||||:||||| ||:||||| :|| | :|||
 Db 1 MELGLRWVFLVAFLEGVQCEVQLVESGGGLVKPGGSLRLSCAASGLSFSTYAMNWVRQAP 60
 QY 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
 | |||:|| | || :||| |||:|||:|||:|||:||| :|||:|| | |
 Db 61 GKGLEWVSSISSRSDYIYYRDSVKGRFTISRDNAKNSLYLQMNSLRVDDTAVYYCAR-DS 119
 QY 121 YSGSSDY----WGQGTTVTVSS 138
 :|: | |||| ||||
 Db 120 CNGAICYGFSPWGQGLVTVSS 141

RESULT 13

Q7Z5W1

ID Q7Z5W1 PRELIMINARY; PRT; 470 AA.
 AC Q7Z5W1;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RA Strausberg R.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC053984; AAH53984.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 470 AA; 51204 MW; 778CF34521483E1A CRC64;

Query Match 62.4%; Score 449; DB 4; Length 470;
 Best Local Similarity 63.8%; Pred. No. 3e-35;
 Matches 90; Conservative 20; Mismatches 27; Indels 4; Gaps 3;

Qy 1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
 | ||| :|||::|:|||||:|||||||:| | ||:| | |||| :| | ||||
 Db 1 MELGLSWVFLVVILEGVQCEVQLVESGGGLVQPGGSLRLSCVASGFTLNNDYDMHWVRQGI 60

 Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSSLKSEDTALYYCVR-YD 119
 | ||||: | : | | ||: ||||| |||||: ||| ||: || | | ||| |
 Db 61 GKGLEWVSKIGTAGDR-YYAGSVKGRFTISRENAKDSLYLQMNSLRVGDAAVYYCARGAG 119

 Qy 120 HYS--GSSDYWGQGT TVTVSS 138
 :: | : | |||| |||||
 Db 120 RWAPLGAFDIWGQGTMTVTVSS 140

RESULT 14

Q80ZI7

ID Q80ZI7 PRELIMINARY; PRT; 487 AA.
 AC Q80ZI7;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)

```

DT      01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE      Hypothetical protein.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=FVB/N; TISSUE=Colon;
RA      Strausberg R.;
RL      Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
DR      EMBL; BC049143; AAH49143.1; -.
DR      InterPro; IPR003599; Ig.
DR      InterPro; IPR007110; Ig-like.
DR      InterPro; IPR003597; Ig_c1.
DR      InterPro; IPR003006; Ig_MHC.
DR      InterPro; IPR003596; Ig_v.
DR      Pfam; PF00047; ig; 3.
DR      SMART; SM00409; IG; 3.
DR      SMART; SM00407; IGc1; 3.
DR      SMART; SM00406; IGv; 1.
DR      PROSITE; PS50835; IG_LIKE; 4.
DR      PROSITE; PS00290; IG_MHC; 2.
KW      Hypothetical protein.
SQ      SEQUENCE      487 AA;  53019 MW;  31F2C893900A4D80 CRC64;

```

RESULT 15

RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC024405; AAH24405.1; -.
 DR PIR; B45837; B45837.
 DR MGD; MGI:96446; Igh-4.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; ig; 3.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 469 AA; 51976 MW; 534793F155D05457 CRC64;

Query Match 60.6%; Score 435.5; DB 11; Length 469;
 Best Local Similarity 61.6%; Pred. No. 6.2e-34;
 Matches 90; Conservative 22; Mismatches 25; Indels 9; Gaps 4;

Qy	1	MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS	60
		: : : : : :	
Db	1	MKLWLNWIFLVTLNNGIQCEVNLVESGGGLVQPGGSLRLSCAASGFTFTDYMSWVRQPP	60
Qy	61	DKRLEWVASIR--SGGGRTYYSDNVKGRFTISRANAKNTLYLQMSSLKSEDTALYYCVR-	117
		: : : : : : : : :	
Db	61	GKALEWLGFIRNKANGYTTEYSASVKGRFTISRDNQSILYLQMNALRAEDSATYYCARD	120
Qy	118	----YDHYSGSS-DYWGQGTTVTVSS	138
		: : :	
Db	121	RRSSY-YYSGTSFAYWGQGLVTVSA	145

Search completed: May 17, 2004, 11:32:30
 Job time : 37.2889 secs

OM protein - protein search, using sw model

Run on: May 17, 2004, 11:11:13 ; Search time 10.2222 Seconds
(without alignments)
702.947 Million cell updates/sec

Title: US-10-010-942B-4
Perfect score: 719
Sequence: 1 MNFGLSLIFLVLVLKGVQCE.....DHYSGSSDYWGQTTVTVSS 138

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	512	71.2	117	1	HV54_MOUSE	P18525 mus musculu
2	510	70.9	117	1	HV55_MOUSE	P18526 mus musculu
3	502.5	69.9	136	1	HV16_MOUSE	P01783 mus musculu
4	501	69.7	117	1	HV59_MOUSE	P18530 mus musculu
5	492	68.4	117	1	HV53_MOUSE	P18524 mus musculu
6	484	67.3	117	1	HV58_MOUSE	P18529 mus musculu
7	463	64.4	117	1	HV3C_HUMAN	P01764 homo sapien
8	433.5	60.3	116	1	HV05_CARAU	P19181 carassius a
9	427	59.4	142	1	HV01_RAT	P01805 rattus norv
10	426	59.2	144	1	HV26_MOUSE	P01795 mus musculu
11	418.5	58.2	97	1	HV56_MOUSE	P18527 mus musculu
12	417	58.0	121	1	HV3J_HUMAN	P01771 homo sapien
13	414	57.6	98	1	HV57_MOUSE	P18528 mus musculu
14	412.5	57.4	122	1	HV3G_HUMAN	P01768 homo sapien
15	406.5	56.5	116	1	HV3T_HUMAN	P01781 homo sapien
16	402.5	56.0	119	1	HV40_MOUSE	P01810 mus musculu
17	400.5	55.7	119	1	HV37_MOUSE	P01807 mus musculu

18	397.5	55.3	116	1	HV36_MOUSE	P01806	mus musculu
19	396.5	55.1	111	1	HV35_MOUSE	P01804	mus musculu
20	395.5	55.0	119	1	HV38_MOUSE	P01808	mus musculu
21	393	54.7	117	1	HV02_CANFA	P01785	canis famil
22	388	54.0	118	1	HV39_MOUSE	P01809	mus musculu
23	387.5	53.9	122	1	HV20_MOUSE	P01789	mus musculu
24	386	53.7	115	1	HV32_MOUSE	P01801	mus musculu
25	385.5	53.6	122	1	HV3A_HUMAN	P01762	homo sapien
26	385	53.5	113	1	HV30_MOUSE	P01799	mus musculu
27	384.5	53.5	126	1	HV3K_HUMAN	P01772	homo sapien
28	384	53.4	119	1	HV3L_HUMAN	P01773	homo sapien
29	382.5	53.2	122	1	HV21_MOUSE	P01790	mus musculu
30	382	53.1	115	1	HV3F_HUMAN	P01767	homo sapien
31	381.5	53.1	114	1	HV3B_HUMAN	P01763	homo sapien
32	380.5	52.9	122	1	HV3H_HUMAN	P01769	homo sapien
33	380	52.9	123	1	HV18_MOUSE	P01787	mus musculu
34	379	52.7	113	1	HV27_MOUSE	P01796	mus musculu
35	379	52.7	120	1	HV3E_HUMAN	P01766	homo sapien
36	378	52.6	115	1	HV33_MOUSE	P01802	mus musculu
37	378	52.6	123	1	HV19_MOUSE	P01788	mus musculu
38	378	52.6	123	1	HV22_MOUSE	P01791	mus musculu
39	377	52.4	113	1	HV31_MOUSE	P01800	mus musculu
40	374	52.0	117	1	HV41_MOUSE	P01811	mus musculu
41	373	51.9	113	1	HV28_MOUSE	P01797	mus musculu
42	372	51.7	119	1	HV3I_HUMAN	P01770	homo sapien
43	372	51.7	123	1	HV23_MOUSE	P01792	mus musculu
44	371	51.6	117	1	HV42_MOUSE	P01812	mus musculu
45	371	51.6	123	1	HV24_MOUSE	P01793	mus musculu

ALIGNMENTS

RESULT 1

HV54_MOUSE

ID HV54_MOUSE STANDARD; PRT; 117 AA.
AC P18525;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 5-84 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/cJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR; JT0505; HVMS84.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.

FT	SIGNAL	1	19	
FT	CHAIN	20	117	IG HEAVY CHAIN V REGION 5-84.
FT	DOMAIN	20	49	FRAMEWORK-1.
FT	DOMAIN	50	54	COMPLEMENTARITY-DETERMINING-1.
FT	DOMAIN	55	68	FRAMEWORK-2.
FT	DOMAIN	69	85	COMPLEMENTARITY-DETERMINING-2.
FT	DOMAIN	86	117	FRAMEWORK-3.
FT	DISULFID	41	115	BY SIMILARITY.
FT	NON_TER	117	117	
SO	SEQUENCE	117 AA;	12872 MW;	234055CB6A469861 CRC64;

Qy 1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
 ||||| :|| ||||| :|| |||||
 Db 1 MNFGLSLIFLVLVLKGVLCCEVKLVESGGGLVQPGGSLKLSCAASGFTFSYTSWVRQTP 60

Qy 61 DKRLEWVASIRSGGGRTYYS DNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVR 117
 :||| | :|| | | | | :|| | | | | :|| |
 Db 61 EKRLEWVAYISNGGGSTYYPDTVKGRFTISRDNAKNNLYLQMSSLKSEDTAMYYCAR 117

```

ID      HV55_MOUSE          STANDARD;          PRT;      117 AA.
AC      P18526;
DT      01-NOV-1990 (Rel. 16, Created)
DT      01-NOV-1990 (Rel. 16, Last sequence update)
DT      15-JUL-1999 (Rel. 38, Last annotation update)
DE      Ig heavy chain V region 345 precursor.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=BALB/cJ;
RX      MEDLINE=89279149; PubMed=2499654;
RA      Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT      "Early onset of somatic mutation in immunoglobulin VH genes during
RT      the primary immune response.";
RL      J. Exp. Med. 169:2007-2019(1989).
CC      -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR      PIR; JT0502; HVMS34.
DR      HSSP; P01810; 2FBJ.
DR      InterPro; IPR007110; Ig-like.
DR      InterPro; IPR003596; Ig_v.
DR      Pfam; PF00047; ig; 1.
DR      SMART; SM00406; IGv; 1.
DR      PROSITE; PS50835; IG LIKE; 1.

```

KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION 345.
 FT DOMAIN 20 49 FRAMEWORK-1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 55 68 FRAMEWORK-2.
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 86 117 FRAMEWORK-3.
 FT DISULFID 41 115 BY SIMILARITY.
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 12902 MW; 49380E4627ACA99A CRC64;

Query Match 70.9%; Score 510; DB 1; Length 117;
 Best Local Similarity 83.8%; Pred. No. 2.2e-44;
 Matches 98; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

Qy 1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
 ||||| ||||| ||||:||||:||||||| ||||| |||||
 Db 1 MNFGLRLIFLVLTLKGVKCEVQLVESGGGLVKPGGSLKLSCAASGFAFSSYDMSWVRQTP 60
 Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRANAKNTLYLQMSSLKSEDTALYYCVR 117
 :||||| | |||| || | |||||:|||||:|||||
 Db 61 EKRLEWVAYISSGGGSTYYPDTVKGRFTISRANAKNTLYLQMSSLKSEDTAMYYCAR 117

RESULT 3

HV16_MOUSE

ID HV16_MOUSE STANDARD; PRT; 136 AA.
 AC P01783;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V region MOPC 21 precursor (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=81234548; PubMed=6788376;
 RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
 RA Baltimore D.;
 RT "Heavy chain variable region contribution to the NPb family of
 RT antibodies: somatic mutation evident in a gamma 2a variable region."
 RL Cell 24:625-637(1981).
 RN [2]
 RP SEQUENCE OF 17-136.
 RX MEDLINE=77100368; PubMed=401950;
 RA Adetugbo K., Milstein C., Secher D.S.;
 RT "Molecular analysis of spontaneous somatic mutants."
 RL Nature 265:299-304(1977).
 CC

 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; J00522; AAD15290.1; -.
 DR PIR; E90809; G1MS21.
 DR PDB; 1IGC; 03-JUN-95.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; ig; 1.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region; Signal; 3D-structure.
 FT NON_TER 1 1
 FT SIGNAL <1 16
 FT CHAIN 17 136 IG HEAVY CHAIN V REGION MOPC 21.
 FT DOMAIN 115 119 D SEGMENT.
 FT DOMAIN 120 136 JH4 SEGMENT.
 FT DISULFID 38 112
 FT CONFLICT 75 78 HYAD -> DYAH (IN REF. 2).
 FT CONFLICT 89 90 DN -> ND (IN REF. 2).
 FT CONFLICT 115 115 W -> H (IN REF. 2).
 FT CONFLICT 120 120 Y -> W (IN REF. 2).
 FT NON_TER 136 136
 SQ SEQUENCE 136 AA; 15071 MW; 2276A98DBDBF7016 CRC64;

Query Match 69.9%; Score 502.5; DB 1; Length 136;
 Best Local Similarity 70.4%; Pred. No. 1.5e-43;
 Matches 95; Conservative 20; Mismatches 19; Indels 1; Gaps 1;

Qy 5 LSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNSDKRL 64
 |:|:||||:|||||:|:|||||||:| | |||||:|:| | ||| :| |
 Db 2 LNLVFLVLILKGVQCDVQLVESGGGLVQPGGSRKLSCAASGFTFSFQGMHWVRQAPEKGL 61
 Qy 65 EWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSLKS EDTALYYCVRYDHYS-G 123
 |||| | || :|:| |||||:| |||:|:|:|:|:| | :| |
 Db 62 EWVAYISSGSTLHYADTVKGRFTISRDNPKNTLFLQMTSLRSED TAMYYCARWGNYPY 121
 Qy 124 SSDYWGQGT TVTVSS 138
 : |||||:|||||
 Db 122 AMDYWGQGT SVTVSS 136

RESULT 4

HV59_MOUSE

ID HV59_MOUSE STANDARD; PRT; 117 AA.
 AC P18530;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V region 7-39 precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/cJ;


```

DR      InterPro; IPR007110; Ig-like.
DR      InterPro; IPR003596; Ig_v.
DR      Pfam; PF00047; ig; 1.
DR      SMART; SM00406; IGv; 1.
DR      PROSITE; PS50835; IG_LIKE; 1.
KW      Immunoglobulin V region; Signal.
FT      SIGNAL                1          19
FT      CHAIN                 20        117      IG HEAVY CHAIN V REGION 5-76.
FT      DOMAIN                20         49      FRAMEWORK-1.
FT      DOMAIN                50         54      COMPLEMENTARITY-DETERMINING-1.
FT      DOMAIN                55         68      FRAMEWORK-2.
FT      DOMAIN                69         85      COMPLEMENTARITY-DETERMINING-2.
FT      DOMAIN                86        117      FRAMEWORK-3.
FT      DISULFID              41        115      BY SIMILARITY.
FT      NON_TER               117        117
SO      SEQUENCE              117 AA: 12991 MW: 93A04782B78B8FA0 CRC64:

```

RESULT 7

```

ID      HV3C_HUMAN          STANDARD;          PRT;    117 AA.
AC      P01764;
DT      21-JUL-1986 (Rel. 01, Created)
DT      21-JUL-1986 (Rel. 01, Last sequence update)
DT      10-OCT-2003 (Rel. 42, Last annotation update)
DE      Ig heavy chain V-III region VH26 precursor.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=81101090; PubMed=6450418;
RA      Matthyssens G., Rabbitts T.H.;
RT      "Structure and multiplicity of genes for the human immunoglobulin
RT      heavy chain variable region.";
RL      Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980).
CC      -!- SIMILARITY: Contains 1 immunoglobulin-like domain.

```

CC or send an email to license@isb-sib.ch).

CC -----
DR EMBL; J00236; AAA53516.1; -.
DR EMBL; M35415; AAA58735.1; -.
DR PIR; A02047; H3HU26.
DR PDB; 1HOU; 23-DEC-99.
DR Genew; HGNC:5545; IGHV@.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal; 3D-structure.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V-III REGION VH26.
FT DOMAIN 20 >117 IG-LIKE.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12582 MW; E826733F1A3CB0F1 CRC64;

Query Match 64.4%; Score 463; DB 1; Length 117;
Best Local Similarity 72.6%; Pred. No. 1.2e-39;
Matches 85; Conservative 17; Mismatches 15; Indels 0; Gaps 0;

QY 1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
| |||| :||| :|||||||:|:|||||||:| | ||:|||||||:| |||||
Db 1 MEFGLSWLFLVAILKGVQCEVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAP 60

QY 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVR 117
| ||||:| || ||| |:|||||||:|:|||||||:|:|:||||:| | :
Db 61 GKGLEWVSAISGGSGSTYYGDSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAK 117

RESULT 8

HV05_CARAU

ID HV05_CARAU STANDARD; PRT; 116 AA.
AC P19181;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 5A precursor.
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OX NCBI_TaxID=7957;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88144476; PubMed=3125551;
RA Wilson M.R., Middleton D., Warr G.W.;
RT "Immunoglobulin heavy chain variable region gene evolution: structure
RT and family relationships of two genes and a pseudogene in a teleost
RT fish."
RL Proc. Natl. Acad. Sci. U.S.A. 85:1566-1570(1988).
DR HSSP; P01772; 2FB4.

DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; ig; 1.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region; Signal.

FT SIGNAL 1 19
 FT CHAIN 20 116 IG HEAVY CHAIN V REGION 5A.
 FT DOMAIN 20 49 FRAMEWORK-1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 55 68 FRAMEWORK-2.
 FT DOMAIN 69 84 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 85 116 FRAMEWORK-3.
 FT DISULFID 41 114 BY SIMILARITY.
 FT NON_TER 116 116
 SQ SEQUENCE 116 AA; 12808 MW; 9C2279E2DF199B12 CRC64;

Query Match 60.3%; Score 433.5; DB 1; Length 116;
 Best Local Similarity 71.8%; Pred. No. 1.1e-36;
 Matches 84; Conservative 16; Mismatches 16; Indels 1; Gaps 1;

Qy 1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
 | | || :||| :|||||||:|||||||:| | ||:||||||| | : |||||
 Db 1 MEFWLSWVFLVAILKGVQCEVQLVESGGGLIQPGSLRLSCAASGFTVSSNYMSWVRQPP 60
 Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRRENAKNTLYLQMSSLKSEDTALYYCVR 117
 | ||||: | ||| |||:|:|||||||:|:|||||||:|:|:|:|:| |
 Db 61 GKGLEWVSVIYSGGS-TYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAR 116

RESULT 9

HV01_RAT

ID HV01_RAT STANDARD; PRT; 142 AA.
 AC P01805;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V region IR2 precursor.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83064537; PubMed=6292865;
 RA Hellman L., Pettersson U., Engstroem A., Karlsson T., Bennich H.;
 RT "Structure and evolution of the heavy chain from rat immunoglobulin
 RT E.";
 RL Nucleic Acids Res. 10:6041-6049(1982).
 CC -!- MISCELLANEOUS: THE MRNA WAS ISOLATED FROM AN IGE-SECRETING
 CC IMMUNOCYTOMA THAT ARISES SPONTANEOUSLY IN LOU/C/WSL RATS.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR; A02075; EVRTR2.
 DR HSSP; P01789; 1MCP.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; ig; 1.

DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 142 IG HEAVY CHAIN V REGION IR2.
 FT DOMAIN 20 133 IG-LIKE.
 FT NON_TER 142 142
 SQ SEQUENCE 142 AA; 16024 MW; DE29E6CFE745DF3B CRC64;

Query Match 59.4%; Score 427; DB 1; Length 142;
 Best Local Similarity 58.3%; Pred. No. 6e-36;
 Matches 84; Conservative 23; Mismatches 29; Indels 8; Gaps 3;

Qy 1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
 |: |: |:| :||| |||| | |||||:| |:| ||| | ||||:| | |||
 Db 1 MDLRLTYVFIVAILKGVLCCEVKLEESGGGLVQPGMSVKLSCATSGFTFSDYWMEWVRQAP 60
 Qy 61 .DKRLEWVASIRSGGGR--TYYS DNVKGRFTISRENAKNTLYLQMSLKS EDTALYYCVRY 118
 | |||| | |: || : |||||:| |:| |:| |:| |:| |:| |:| |
 Db 61 GKGLEWVAEIRNKANNYVAYYGKSLKGRFTLSRDDSKSIVYLQMNIRSED TGIYYCSR- 119
 Qy 119 DHYSGSSD----YWGQGT TVTVSS 138
 | | |: | |||| | ||||
 Db 120 -GYGGYSENWFEVYWGQGT LVTVSS 142

RESULT 10
 HV26_MOUSE

ID HV26_MOUSE STANDARD; PRT; 144 AA.
 AC P01795;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V region M167 precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93358330; PubMed=6101208;
 RA Kim S., Davis M., Sinn E., Patten P., Hood L.;
 RT "Antibody diversity: somatic hypermutation of rearranged VH genes."
 RL Cell 27:573-581(1981).
 RN [2]
 RP SEQUENCE OF 20-142.
 RX MEDLINE=76222762; PubMed=819932;
 RA Rudikoff S., Potter M.;
 RT "Size differences among immunoglobulin heavy chains from
 RT phosphorylcholine-binding proteins."
 RL Proc. Natl. Acad. Sci. U.S.A. 73:2109-2112(1976).
 CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGA MYELOMA PROTEIN
 CC THAT BINDS PHOSPHORYLCHOLINE.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

RT the primary immune response.";
 RL J. Exp. Med. 169:2007-2019(1989).
 CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR; JT0504; HVMS91.
 DR HSSP; P01810; 2FBJ.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; ig; 1.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 >97 IG-LIKE.
 FT NON_TER 97 97
 SQ SEQUENCE 97 AA; 10661 MW; C23CB33FF55DA893 CRC64;

Query Match 58.2%; Score 418.5; DB 1; Length 97;
 Best Local Similarity 82.7%; Pred. No. 2.8e-35;
 Matches 81; Conservative 7; Mismatches 9; Indels 1; Gaps 1;

Qy 20 EVKLIVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNSDKRLEWVASIRSGGGRTYY 79
 ||||| :||||| :||||| :|||
 Db 1 EVKLIVESGGGLVKPGGSLKLSCAASGFTFSYAMSWVRQTPEKRLEWVASI-SSGGSTYY 59
 Qy 80 SDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVR 117
 |:|||||:|:| :|||:||||:| |
 Db 60 PDSVKGRFTISRDNARNILYLQMSSLRSEDTAMYYCAR 97

RESULT 12

HV3J_HUMAN

ID HV3J_HUMAN STANDARD; PRT; 121 AA.
 AC P01771;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V-III region HIL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=79124695; PubMed=420800;
 RA Chiu Y.-Y.H., Lopez de Castro J.A., Poljak R.J.;
 RT "Amino acid sequence of the VH region of human myeloma
 RT cryoimmunoglobulin IgG HIL.";
 RL Biochemistry 18:553-560(1979).
 CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA
 CC PROTEIN.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR; A02054; G1HUHL.
 DR HSSP; P01772; 2FB4.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; ig; 1.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region; Pyrrolidone carboxylic acid.
 FT DOMAIN 1 112 IG-LIKE.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT NON_TER 121 121
 SQ SEQUENCE 121 AA; 13566 MW; 480FC53610EF5DAB CRC64;

Query Match 58.0%; Score 417; DB 1; Length 121;
 Best Local Similarity 66.1%; Pred. No. 5e-35;
 Matches 80; Conservative 16; Mismatches 23; Indels 2; Gaps 1;

Qy 20 EVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNSDKRLEWVASIRSGGGRTYY 79
 :||||:||||:|:| | |:||| ||||| |||| | |||| | ||||
 Db 1 QVKLVQAGGGVVQPGRSRLRLSCIASGFTFSNYGMHWVRQAPGKGLEWVAVIYNGSRTYY 60
 Qy 80 SDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDHY--SGSSDYWGQGTTVTVS 137
 |:|||||||:|:| |||:|:|:|:|:| | : | ||||| ||||
 Db 61 GDSVKGRFTISRDNSKRTLYMZMNSLRTEDTAVYYCARDPDILTAFSFDYWGQGVLTVS 120
 Qy 138 S 138
 |
 Db 121 S 121

RESULT 13

HV57_MOUSE

ID HV57_MOUSE STANDARD; PRT; 98 AA.
 AC P18528;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V region 6.96.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/cJ;
 RX MEDLINE=89279149; PubMed=2499654;
 RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
 RT "Early onset of somatic mutation in immunoglobulin VH genes during
 RT the primary immune response.";
 RL J. Exp. Med. 169:2007-2019(1989).
 CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR; JT0501; HVMS96.
 DR HSSP; P01772; 2FB4.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; ig; 1.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region.

FT DOMAIN 1 >98 IG-LIKE.
 FT NON_TER 98 98
 SQ SEQUENCE 98 AA; 11007 MW; B8644F7F92FBF95B CRC64;

Query Match 57.6%; Score 414; DB 1; Length 98;
 Best Local Similarity 80.6%; Pred. No. 7.9e-35;
 Matches 79; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

Qy 20 EVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNSDKRLEWVASIRSGGGRTYY 79
 ||:||||||| ||||| ||||| :||| ||| |||
 Db 1 EVQLVESGGGLVKPGGSLKLSCAASGFTFSDDYMYWVRQTPEKRLEWVATISDGGSYTTY 60
 Qy 80 SDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVR 117
 |:|||||||:|||| ||||| |||||:||| |
 Db 61 PDSVKGRFTISRDNAKNNLYLQMSSLKSEDTAMYYCAR 98

RESULT 14

HV3G_HUMAN

ID HV3G_HUMAN STANDARD; PRT; 122 AA.
 AC P01768;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V-III region CAM.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=81013859; PubMed=6774332;
 RA Lehman D.W., Putnam F.W.;
 RT "Amino acid sequence of the variable region of a human mu chain:
 RT location of a possible JH segment."
 RL Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243(1980).
 CC -!- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM THE PLASMA OF A
 CC PATIENT WITH MACROGLOBULINEMIA.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR; A02051; M3HUAM.
 DR HSSP; P01772; 2FB4.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; ig; 1.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region; Pyrrolidone carboxylic acid.
 FT DOMAIN 1 112 IG-LIKE.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT NON_TER 122 122
 SQ SEQUENCE 122 AA; 13668 MW; A42D0F17D252F1C2 CRC64;

Query Match 57.4%; Score 412.5; DB 1; Length 122;
 Best Local Similarity 64.2%; Pred. No. 1.4e-34;

Matches	79;	Conservative	19;	Mismatches	20;	Indels	5;	Gaps	2;
Qy	20	EVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNSDKRLEWVASIRSGGGRTYY	79						
Db	1	QVELVESGGGVVZPGRSLRLSCAASGFTFSNYAMHWVRQPPGKGLEWVAVISYBGBBKYY	60						
Qy	80	SDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVR----	135						
Db	61	ABSVKGRFTISRDBSKBTLYLQMNSLRAEBTAVYYCARDRLYGBYR-AFNYWQGQGLT	119						
Qy	136	VSS	138						
Db	120	VSS	122						

```

RESULT 15
HV3T_HUMAN
ID HV3T_HUMAN STANDARD; PRT; 116 AA.
AC P01781;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region GAL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=75059123; PubMed=4803843;
RA Watanabe S., Barnikol H.U., Horn J., Bertram J., Hilschmann N.;
RT "The primary structure of a monoclonal IgM-immunoglobulin
RT (macroglobulin Gal.), II: the amino acid sequence of the H-chain (mu-
RT type), subgroup H III. Architecture of the complete IgM-molecule.";
RL Hoppe-Seyler's Z. Physiol. Chem. 354:1505-1509(1973).
RN [2]
RP REVISION TO 28-33.
RA Hilschmann N.;
RL Submitted (JUN-1975) to the PIR data bank.
CC -!- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM A WALDENSTROM'S
CC MACROGLOBULIN.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02064; M3HUGL.
DR HSSP; P01772; 2FB4.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 112 IG-LIKE.
FT NON_TER 116 116
SQ SEQUENCE 116 AA; 12730 MW; 2C67CA9AAAAA1282 CRC64;

```

Query Match 56.5%; Score 406.5; DB 1; Length 116;
Best Local Similarity 67.2%; Pred. No. 5.4e-34;
Matches 80; Conservative 13; Mismatches 23; Indels 3; Gaps 1;

```
Qy      20 EVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNSDKRLEWVASIRSGGGRTYY 79
      ||:||||| ||:| ||:||||||| | : ||:|||| | ||||:|: | |
Db      1 EVQLVESGGDLVQPGRSLRLSCAASGFBFBBLGMTWVRQAPGKGLEWVANIKZBGSZZBY 60

Qy      80 SDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDHYSGSSDYWGQGTTVTVSS 138
      |:|||||||:||||:||||:|: ||||| | | ||||| |||:
Db      61 VDSVKGRFTISRDNAKNSLYLQMNSLRVEDTALYYCAR--GWGGGDYWGQGLVTVST 116
```

Search completed: May 17, 2004, 11:31:05
Job time : 10.2222 secs